

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 1 of 64
Atty. Dkt.: 2551-69

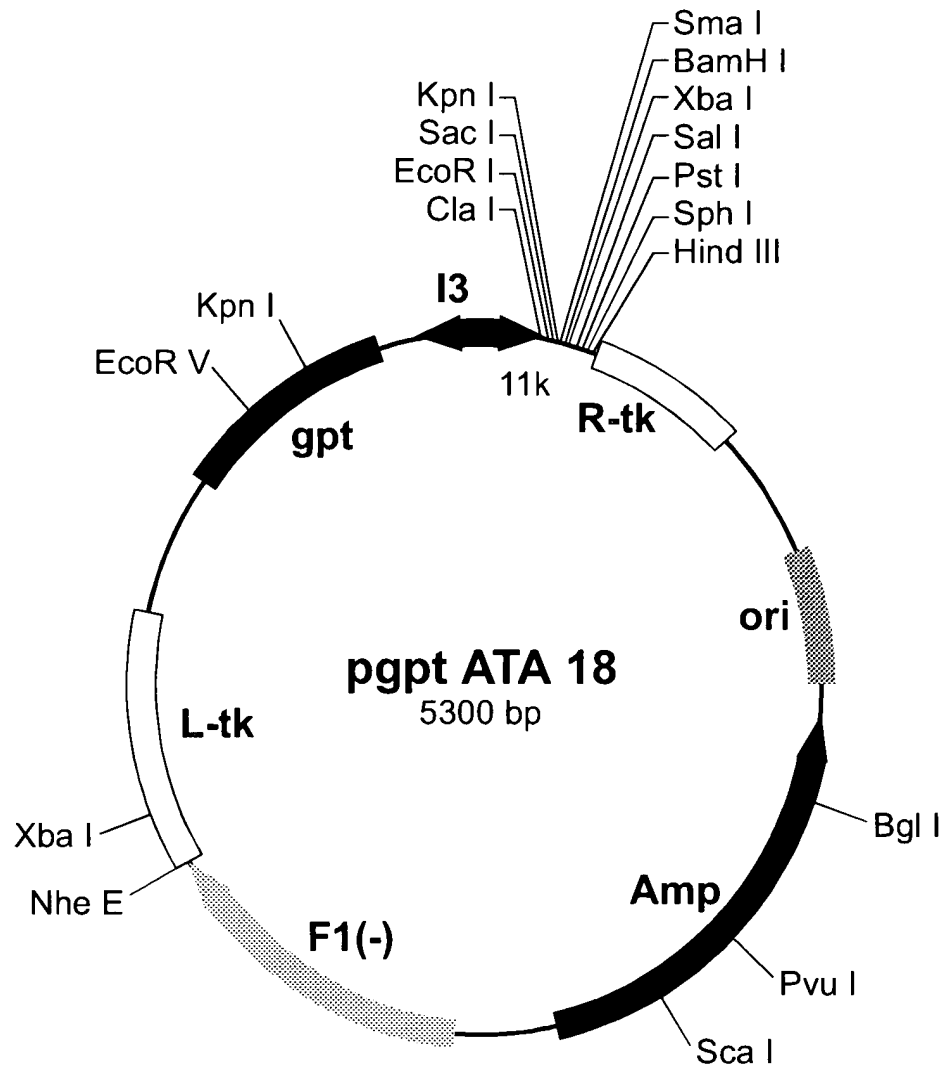


Figure 1

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 2 of 64
 Atty. Dkt.: 2551-69

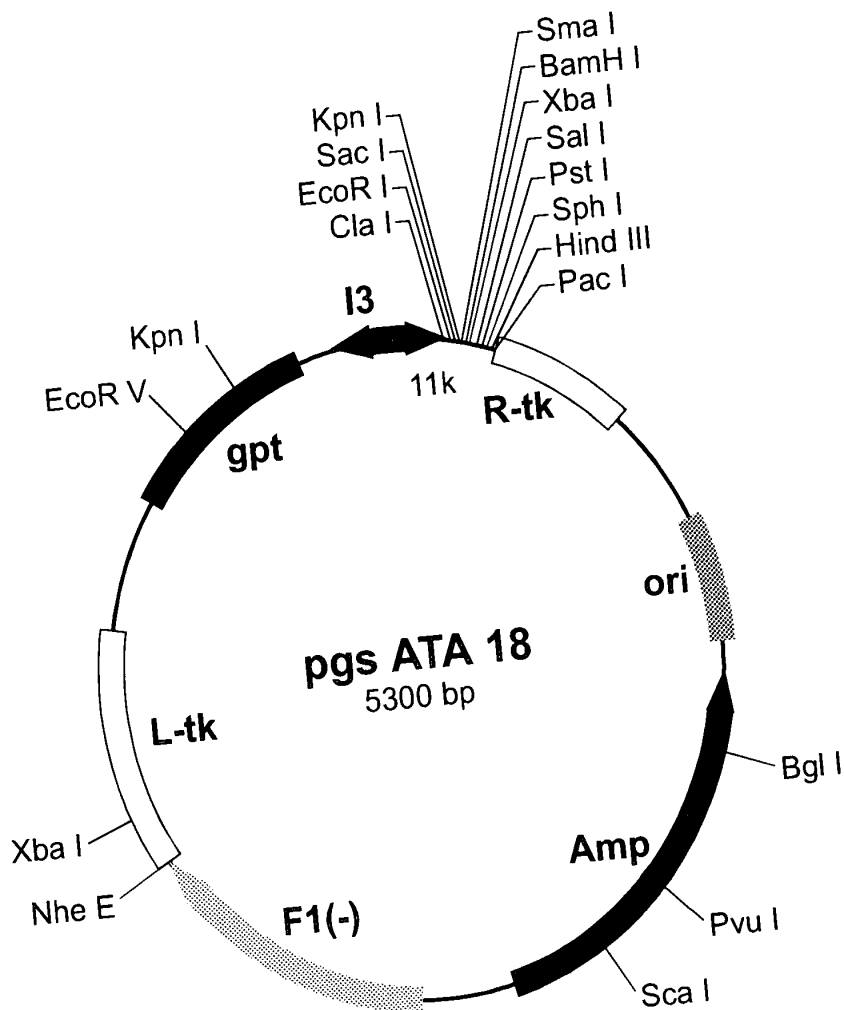


Figure 2



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 3 of 64
Atty. Dkt.: 2551-69

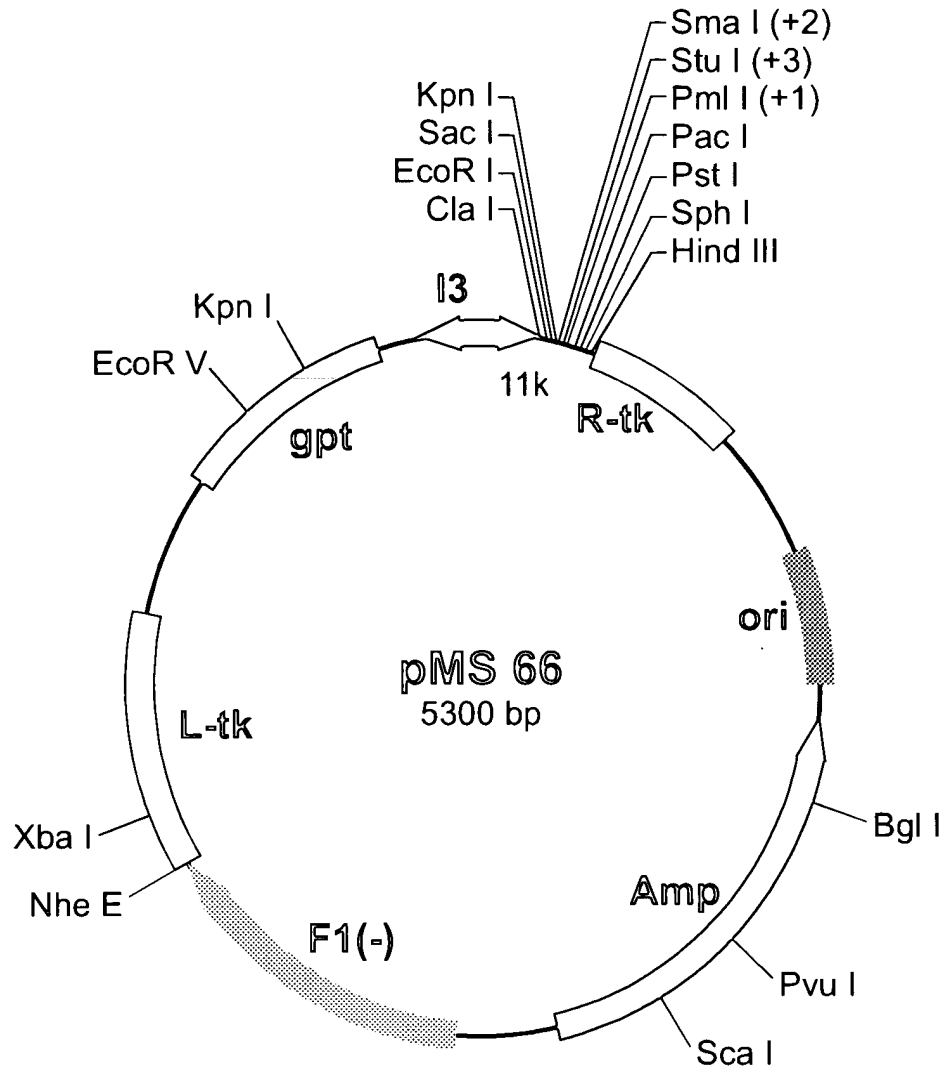


Figure 3

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 4 of 64
Atty. Dkt.: 2551-69

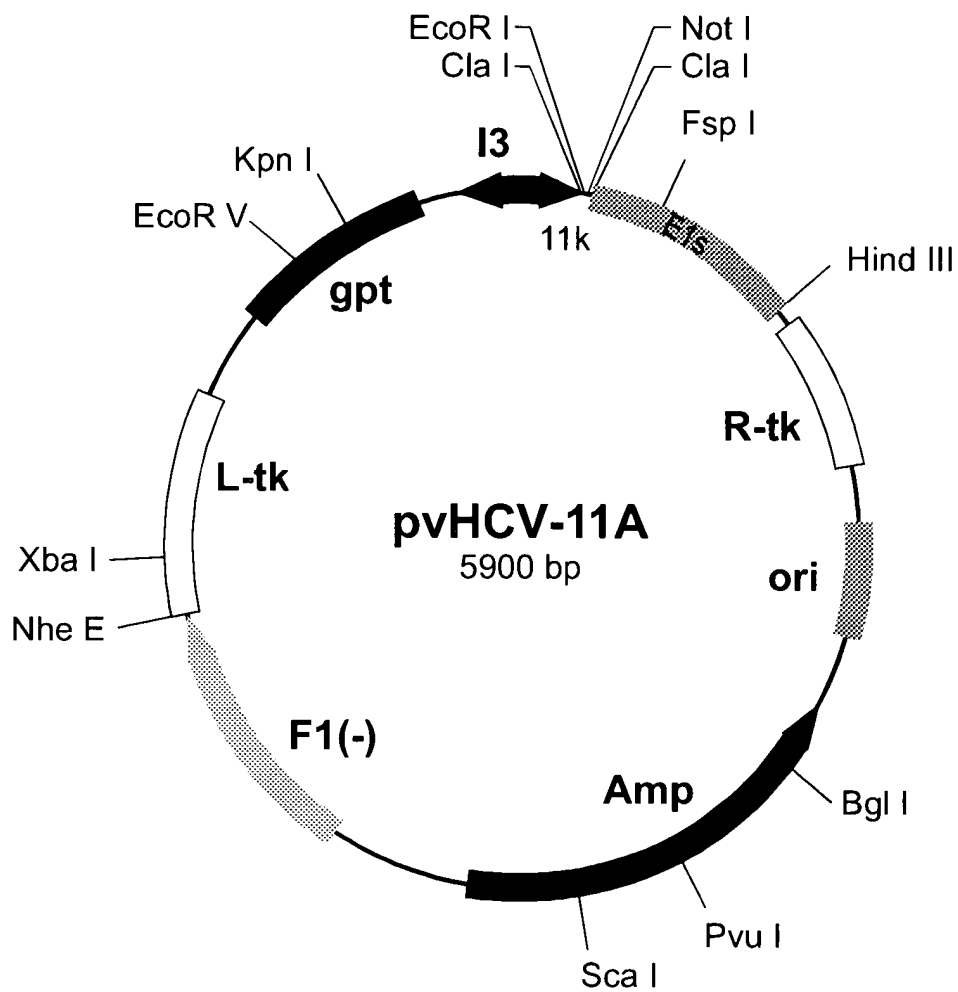


Figure 4

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 5 of 64
 Atty. Dkt.: 2551-69



Anti-E1 levels in NON-responders to IFN treatment

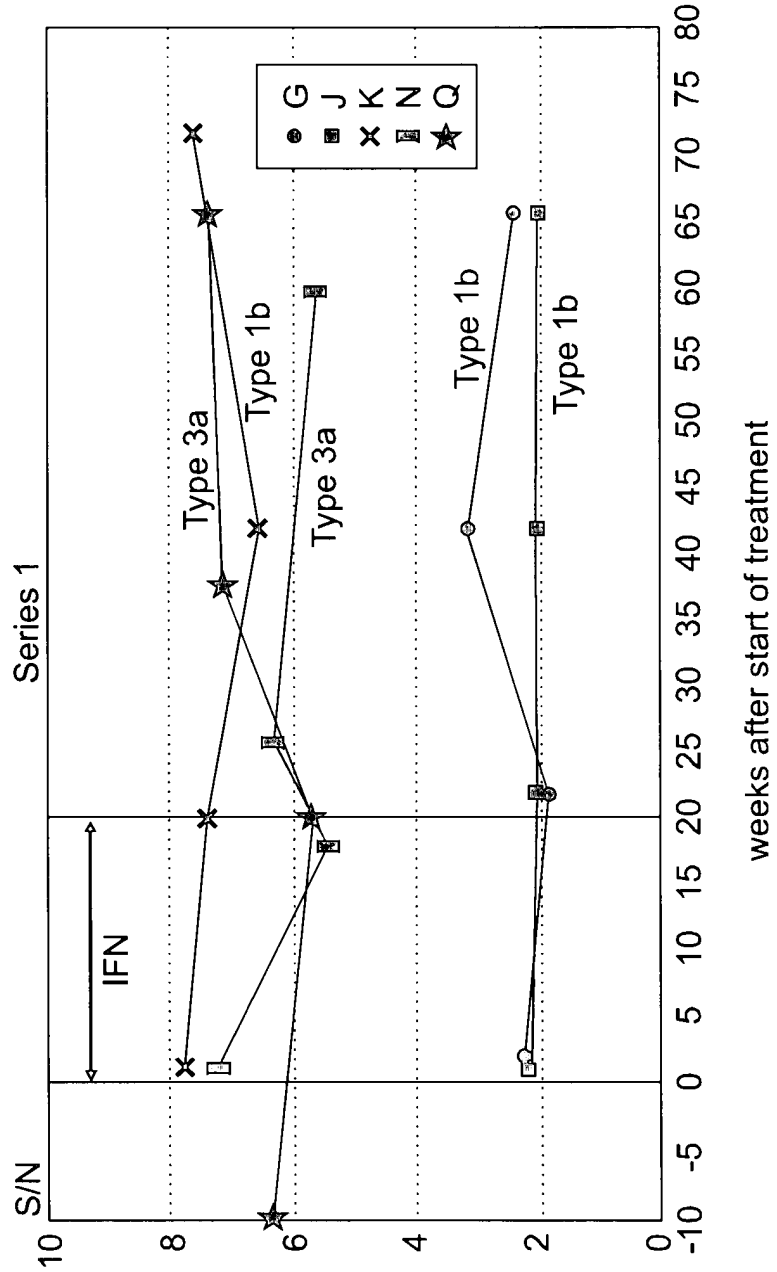


Figure 5

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 6 of 64
 Atty. Dkt.: 2551-69



Anti-E1 levels in RESPONDERS to IFN treatment

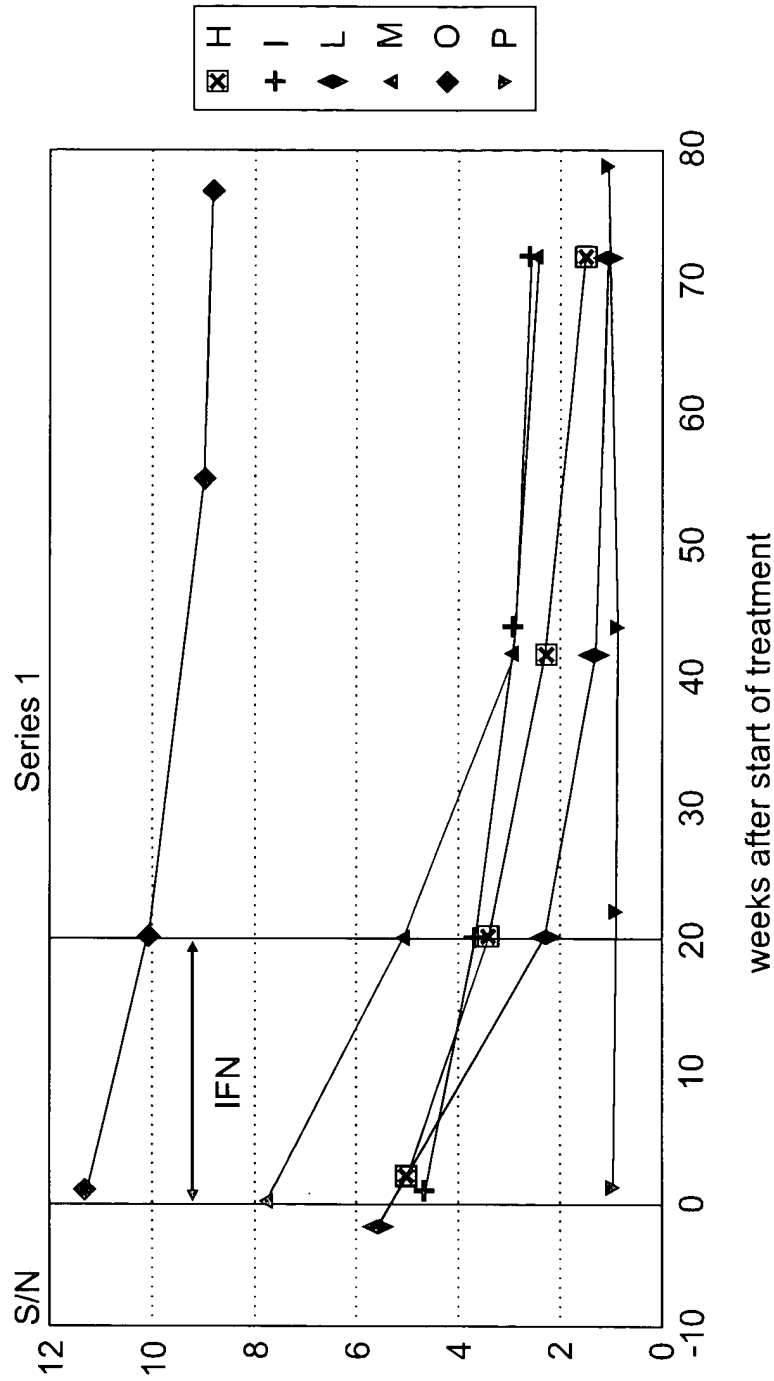


Figure 6

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 7 of 64
 Atty. Dkt.: 2551-69



Anti-E1 levels in patients with COMPLETE response to IFN

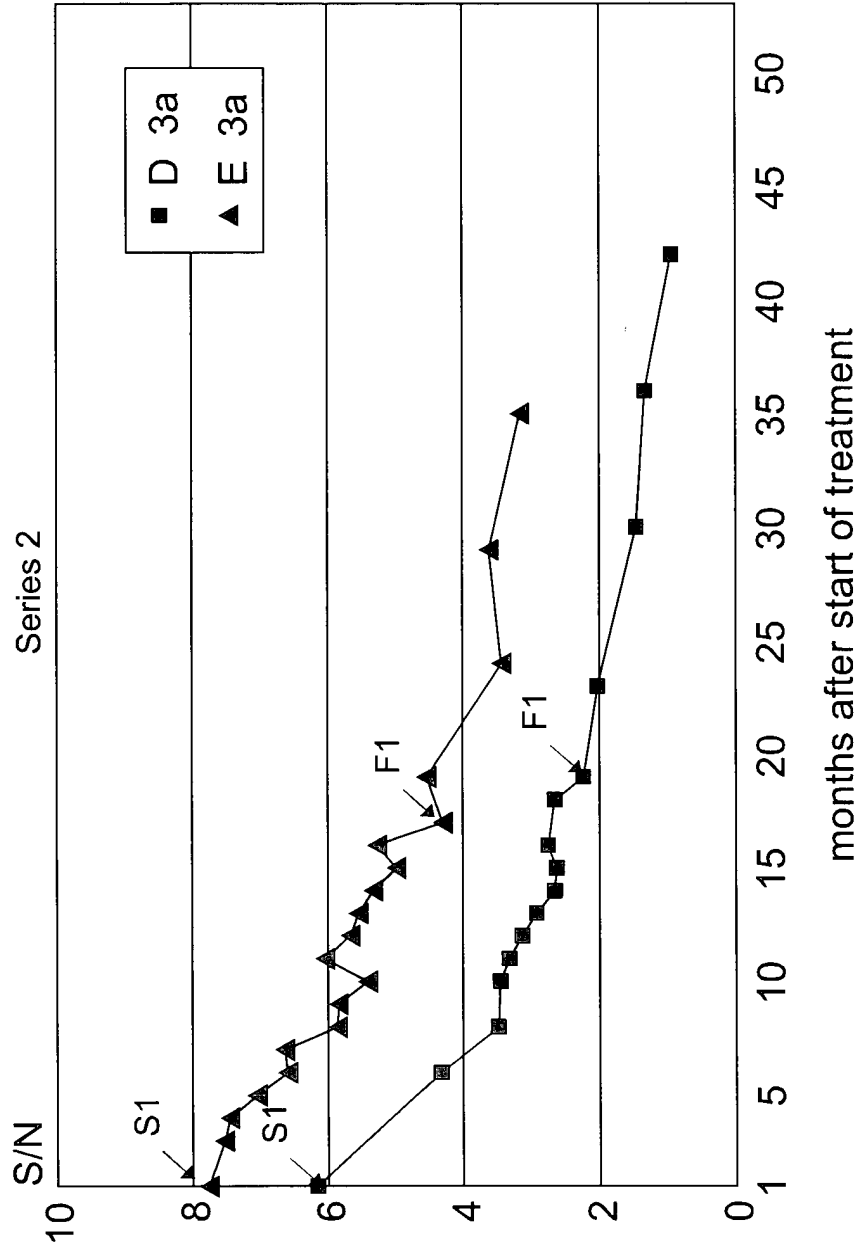


Figure 7

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 8 of 64
 Atty. Dkt.: 2551-69



Anti-E1 levels in INCOMPLETE responders to IFN treatment

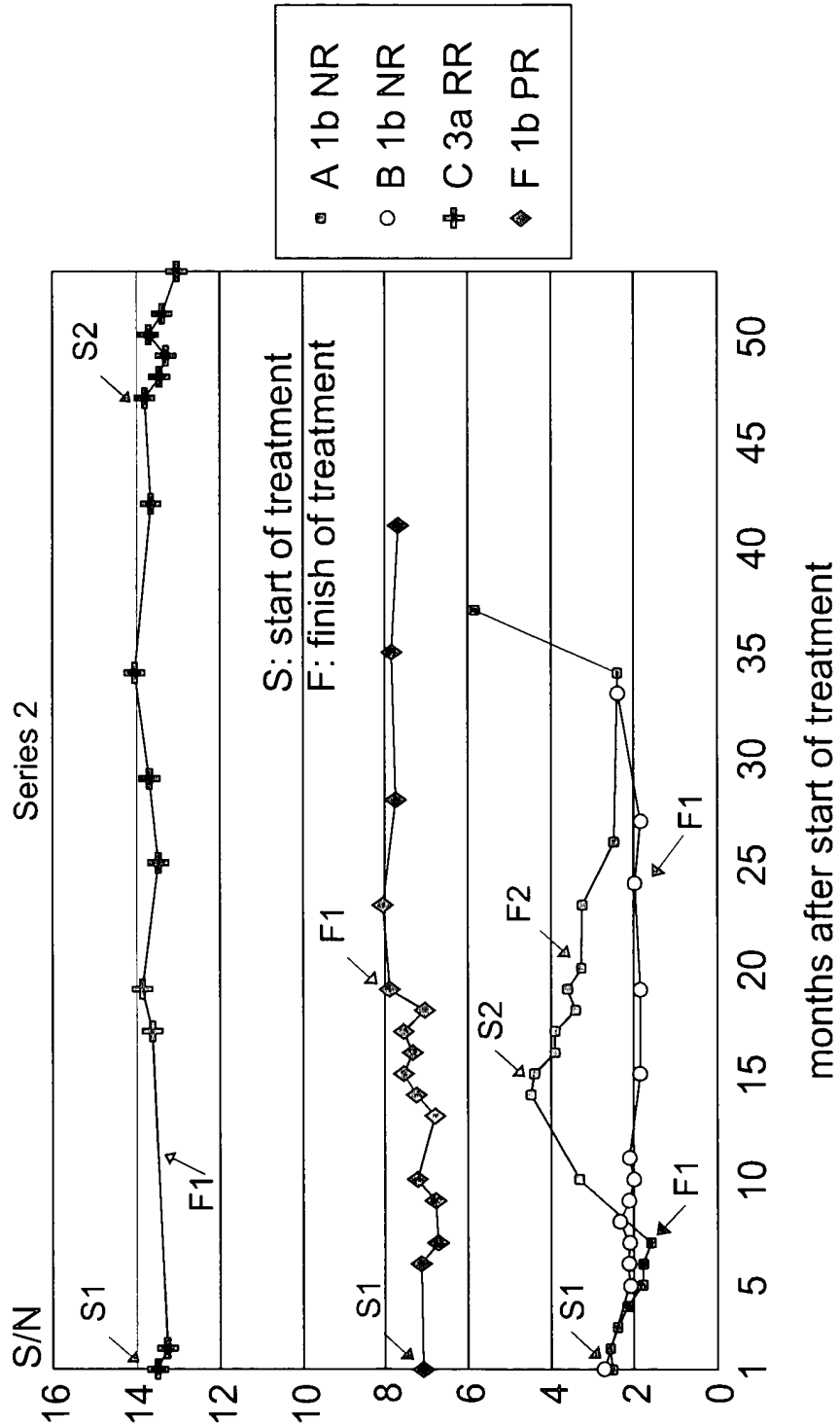


Figure 8

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 9 of 64
Atty. Dkt.: 2551-69



Anti-E2 levels in RESPONDERS to IFN treatment

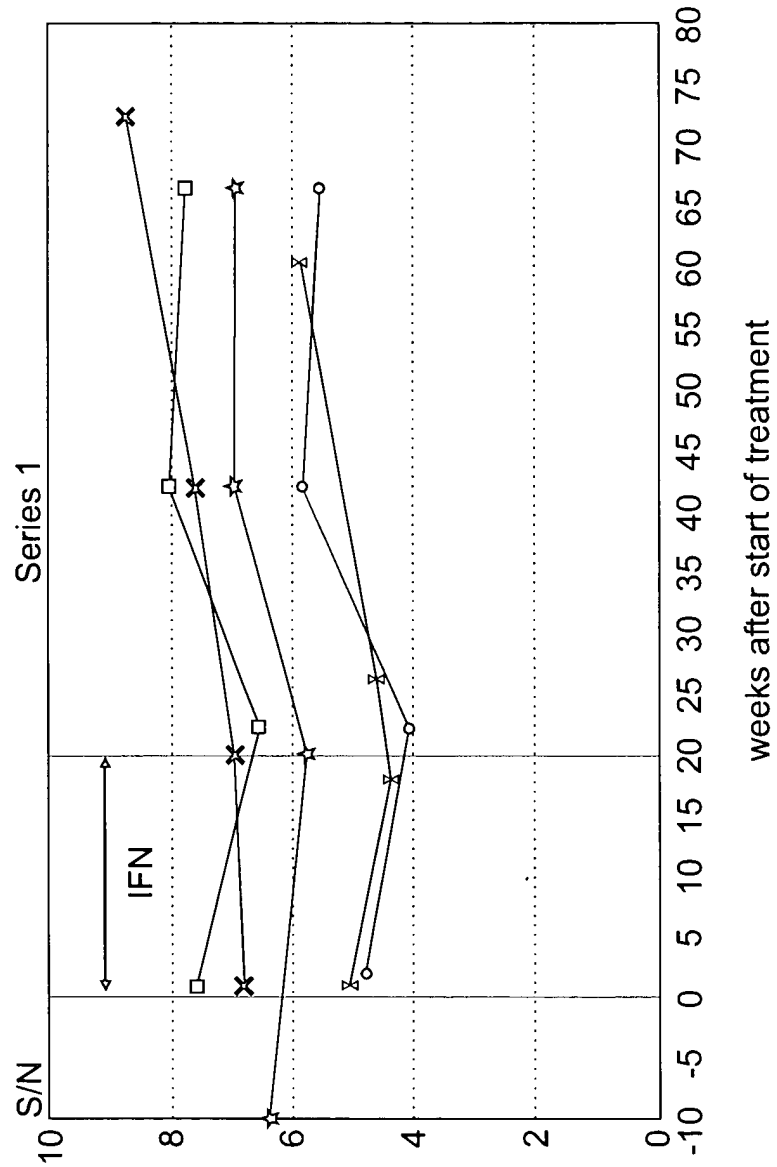


Figure 9

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 10 of 64
Atty. Dkt.: 2551-69



Anti-E2 levels in RESPONDERS to IFN treatment

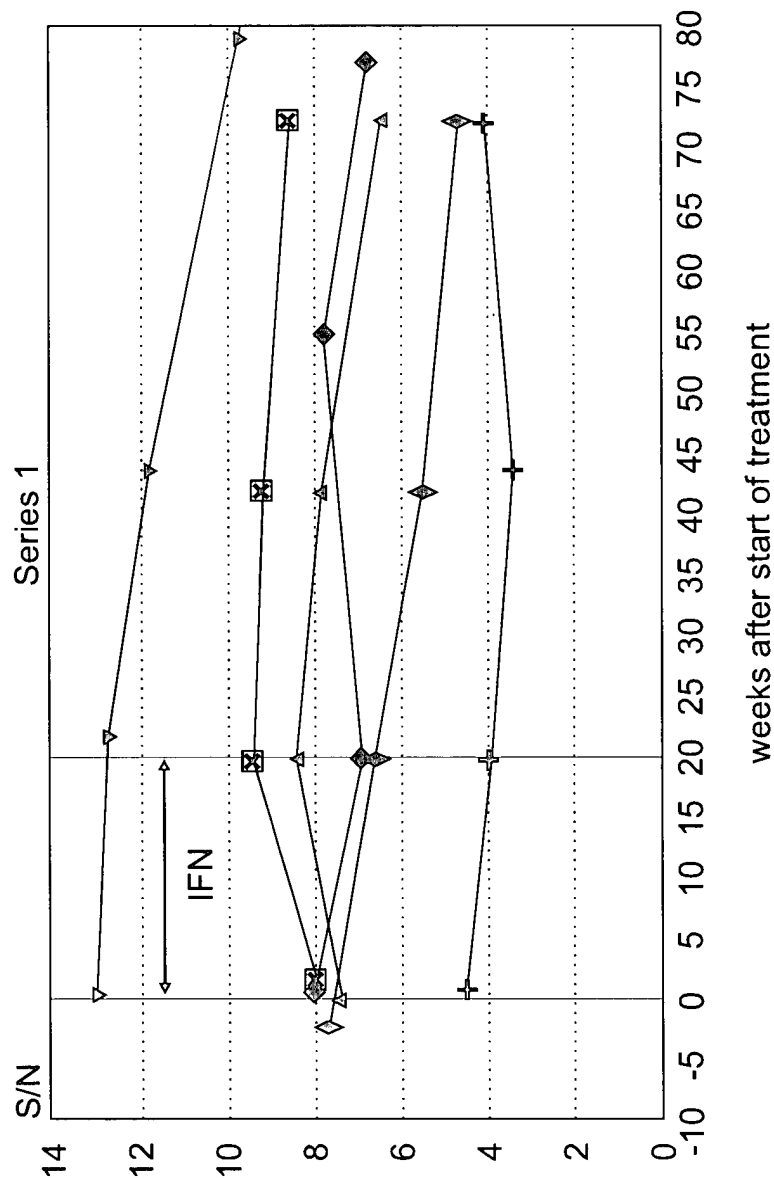


Figure 10

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 11 of 64
Atty. Dkt.: 2551-69



Anti-E2 levels in INCOMPLETE responders to IFN treatment

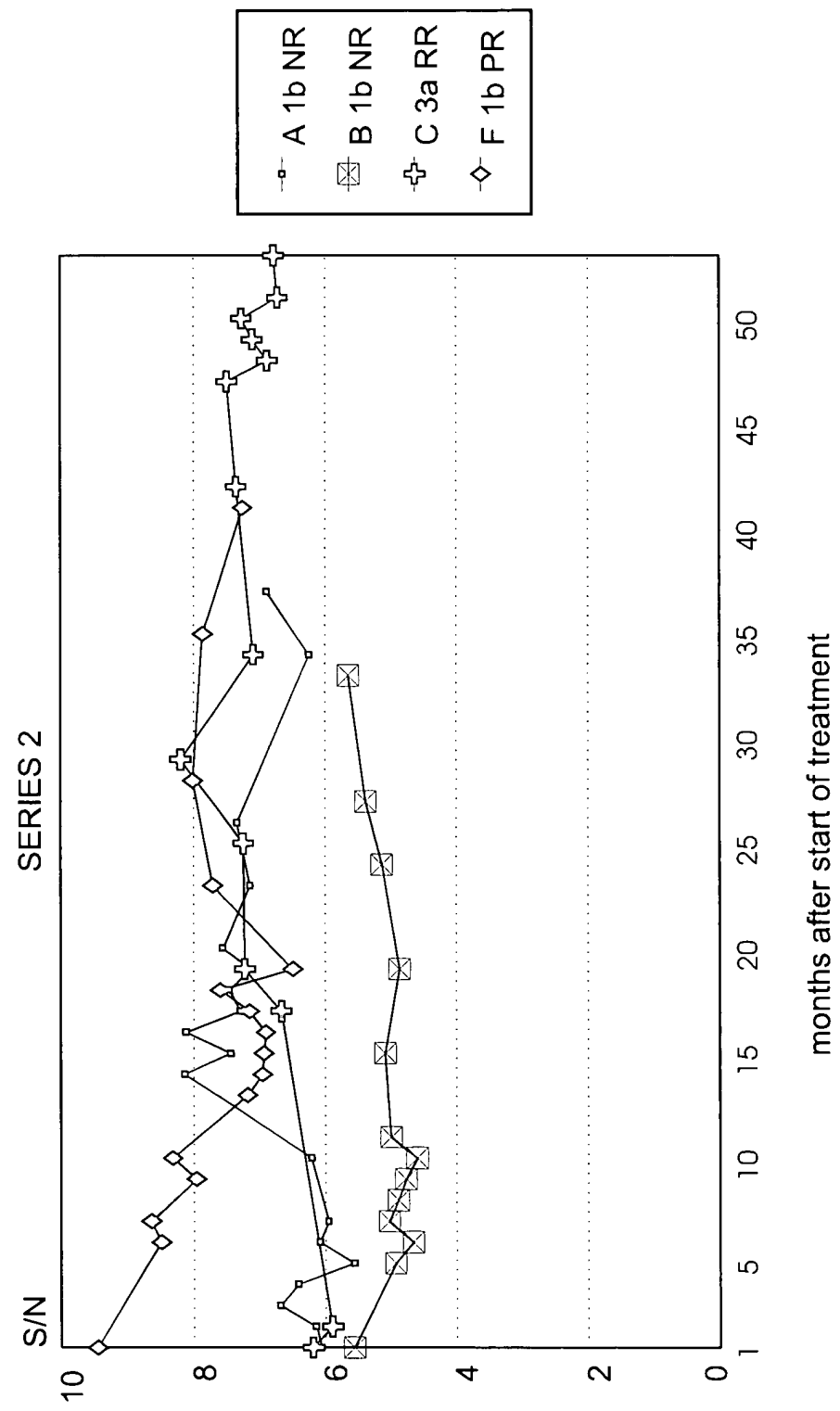


Figure 11



Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 12 of 64
 Atty. Dkt.: 2551-69

09/995,860, 072902

Anti-E2 levels in COMPLETE responders to IFN treatment

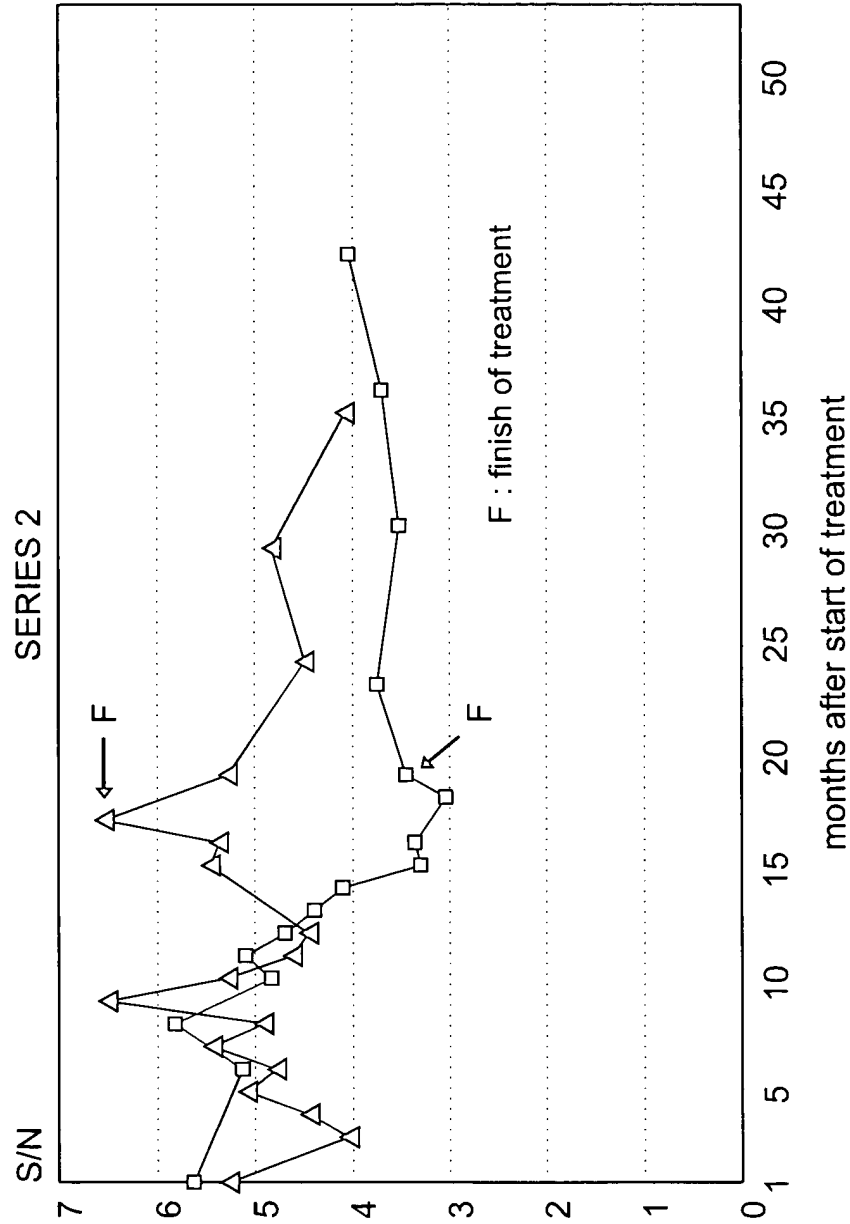


Figure 12

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 13 of 64
 Atty. Dkt.: 2551-69



Human anti-E1 reactivity competed with peptides

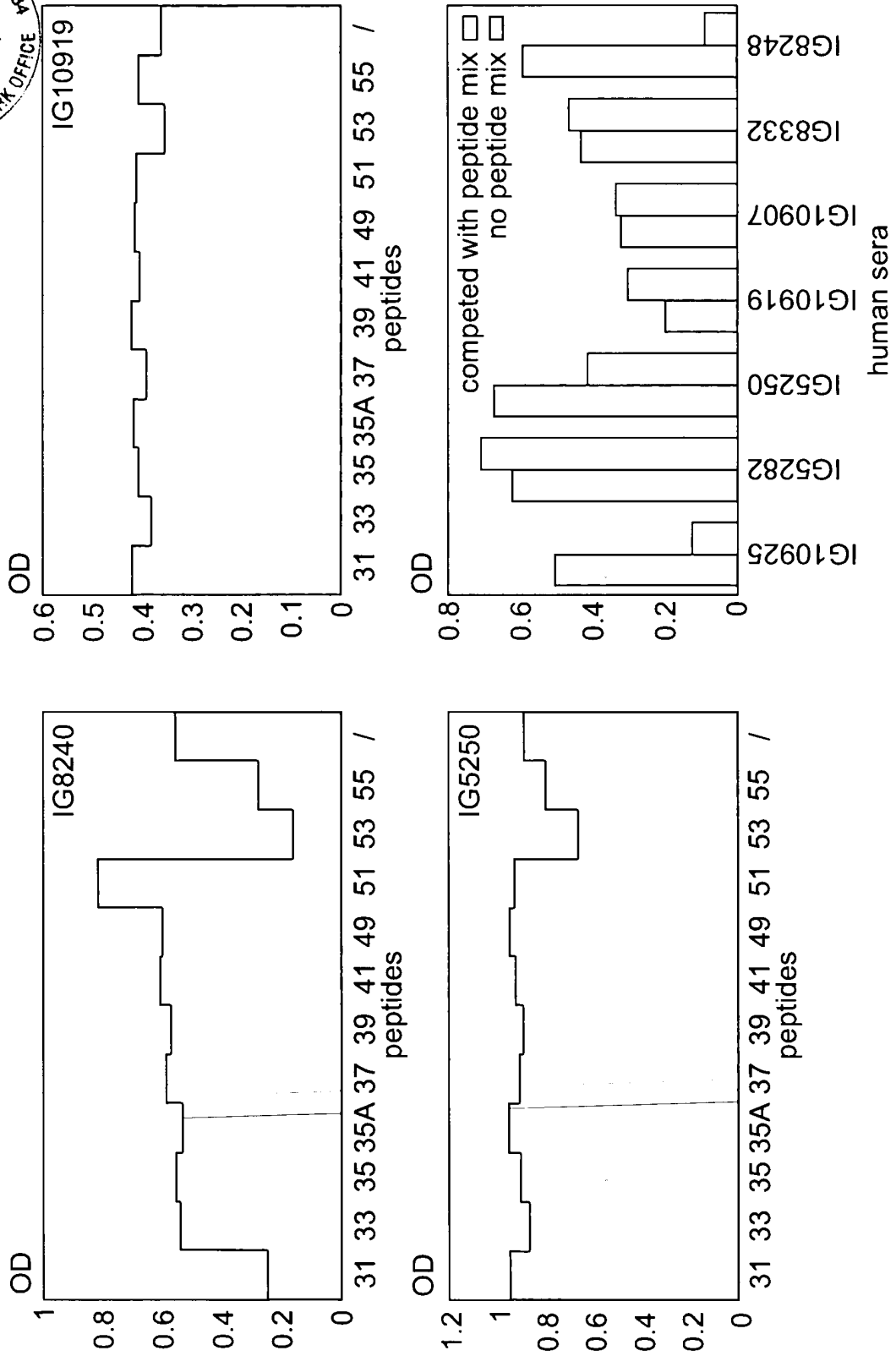


Figure 13

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 14 of 64
 Atty. Dkt.: 2551-69



Competition of reactivity of anti-E1 Mabs with peptides

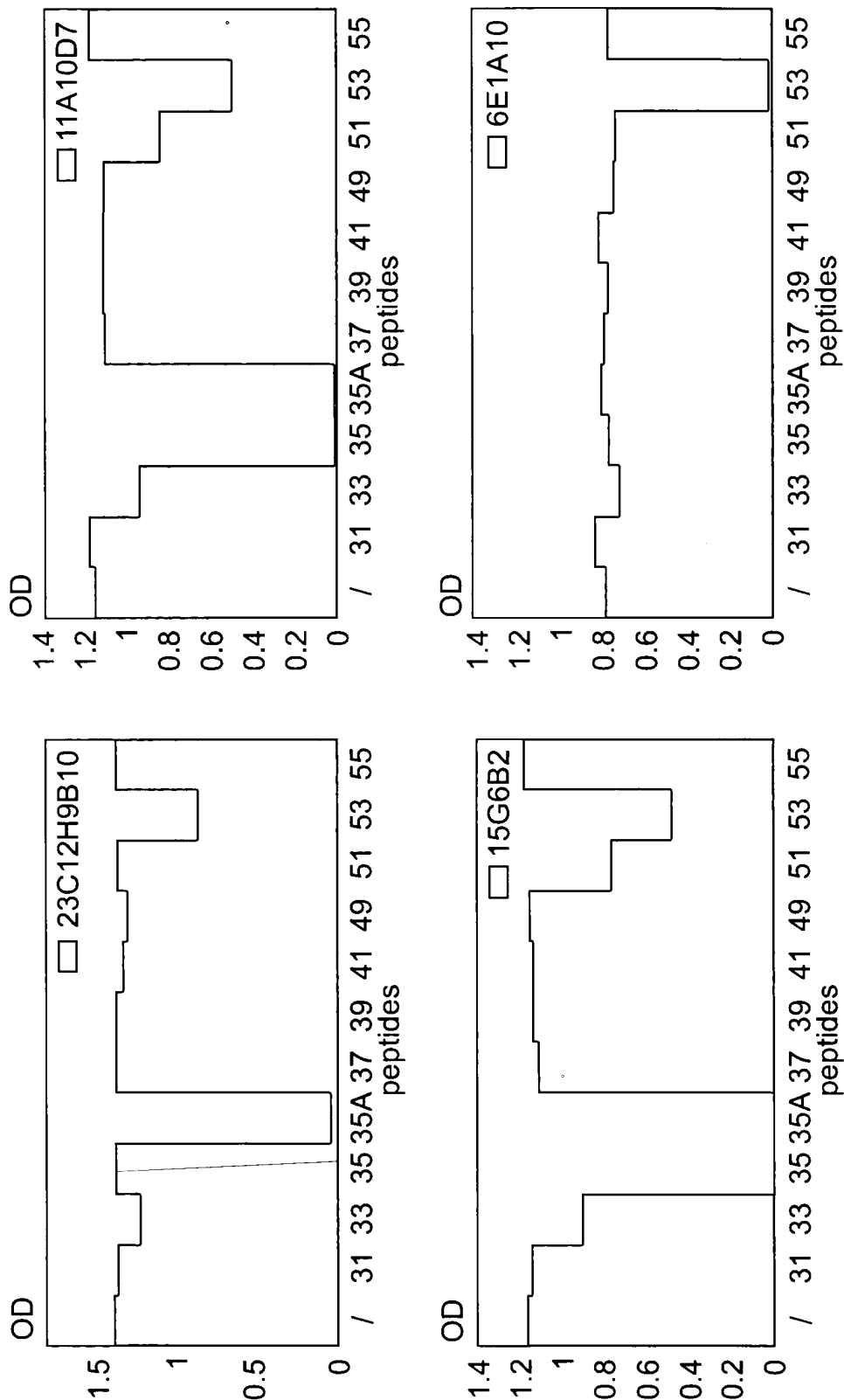


Figure 14

Inventor: MAERTENS, et al.
 SN 09/95,860/Sheet 15 of 64
 Atty. Dkt.: 2551-69



Anti-E1 (epitope 1) levels in NON-RESPONDERS to IFN treatment

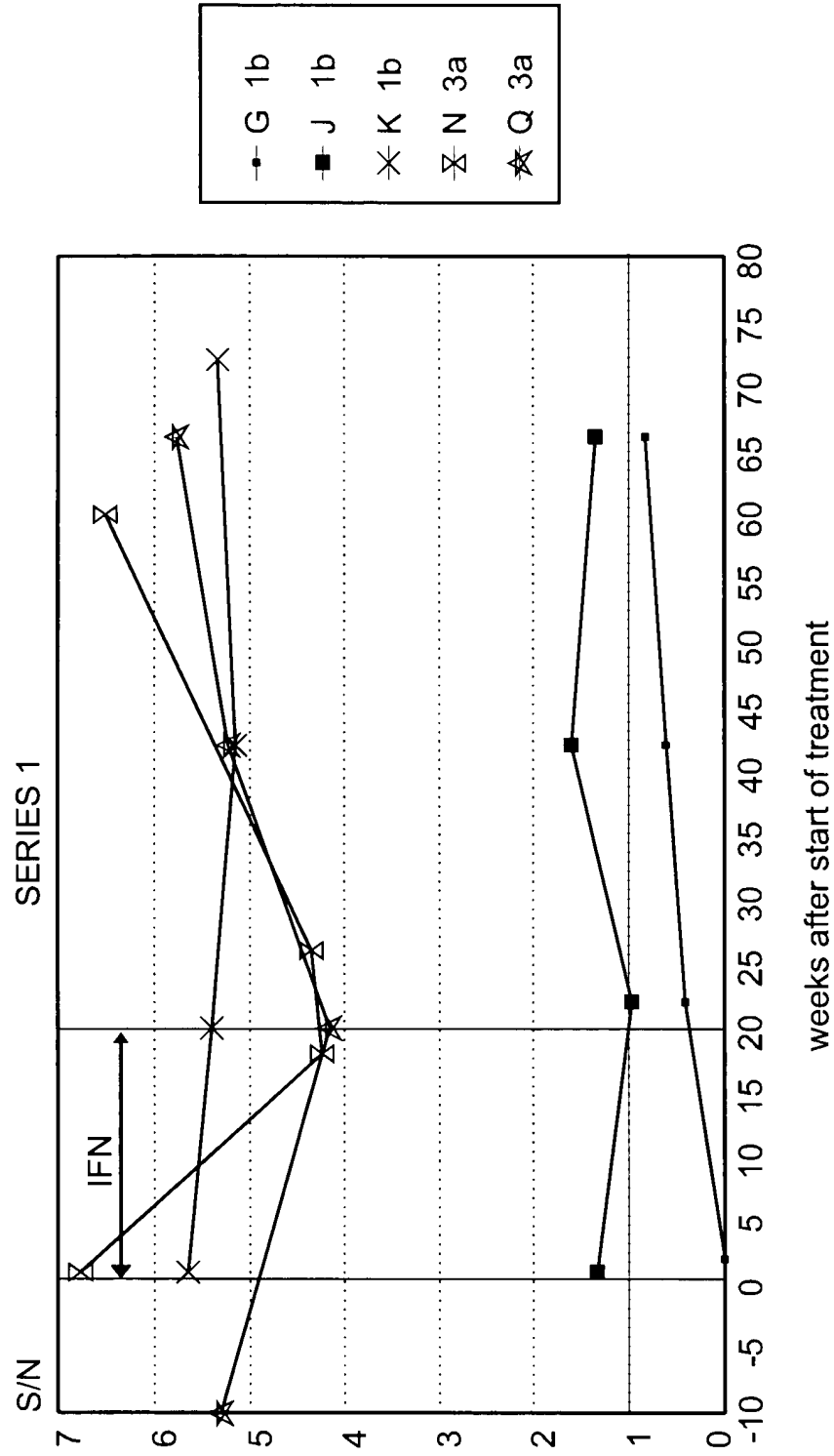


Figure 15

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 16 of 64
 Atty. Dkt.: 2551-69



Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment

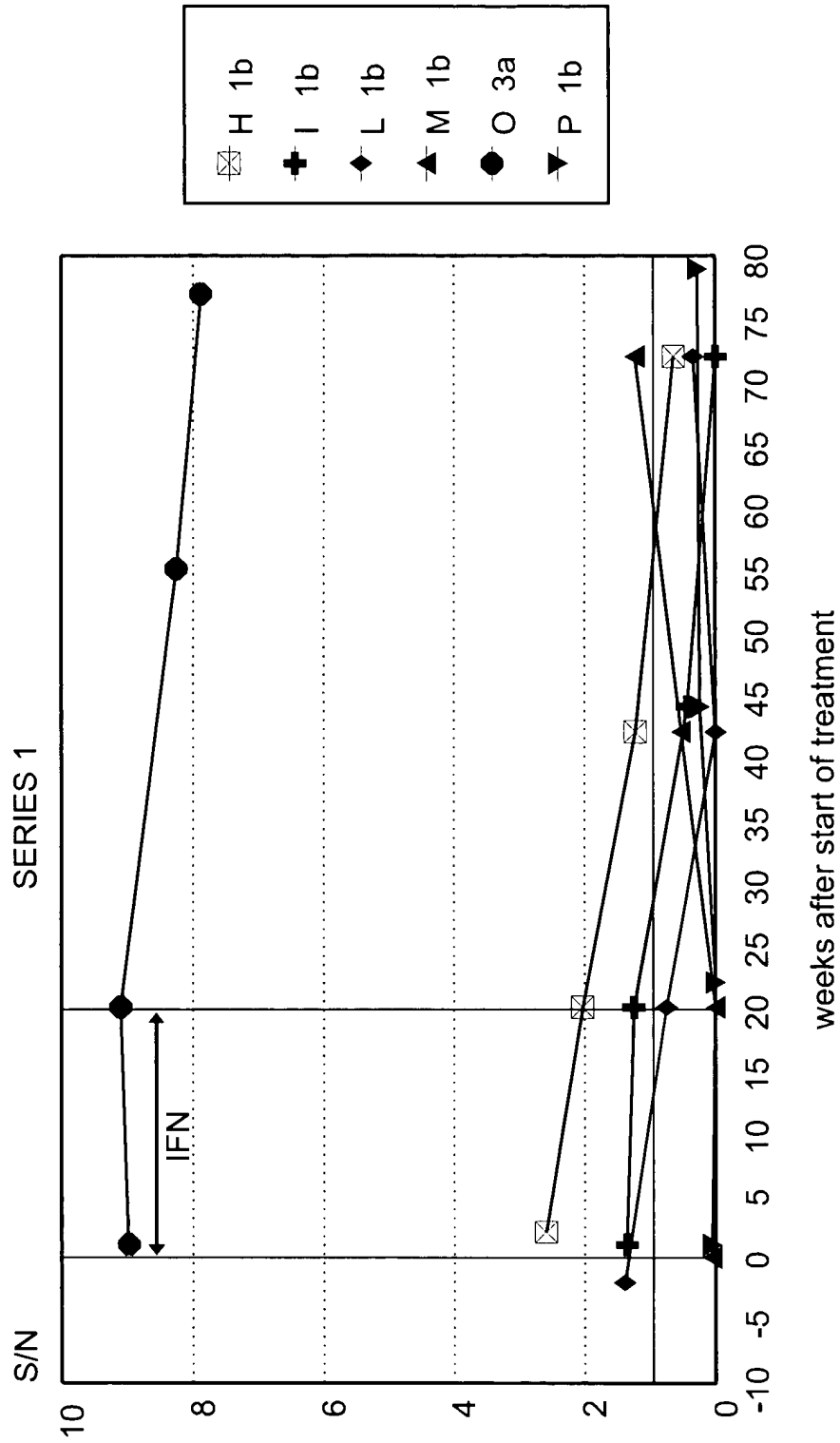


Figure 16

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 17 of 64
 Atty. Dkt.: 2551-69



Anti-E1 (epitope 2) levels in NON-RESPONDERS to IFN treatment

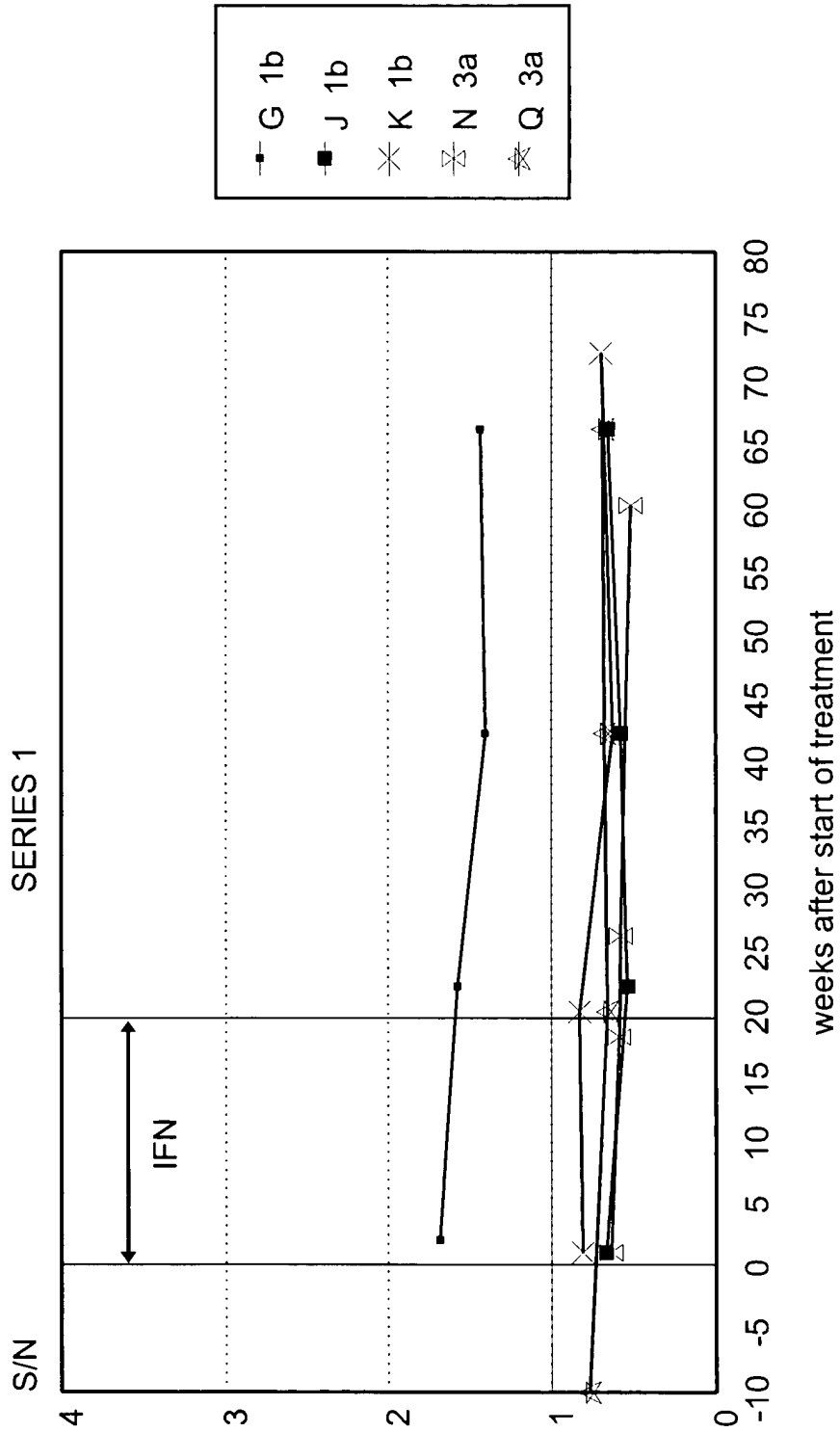


Figure 17

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 18 of 64
Atty. Dkt.: 2551-69



Anti-E1 (epitope 2) levels in RESPONDERS to IFN treatment

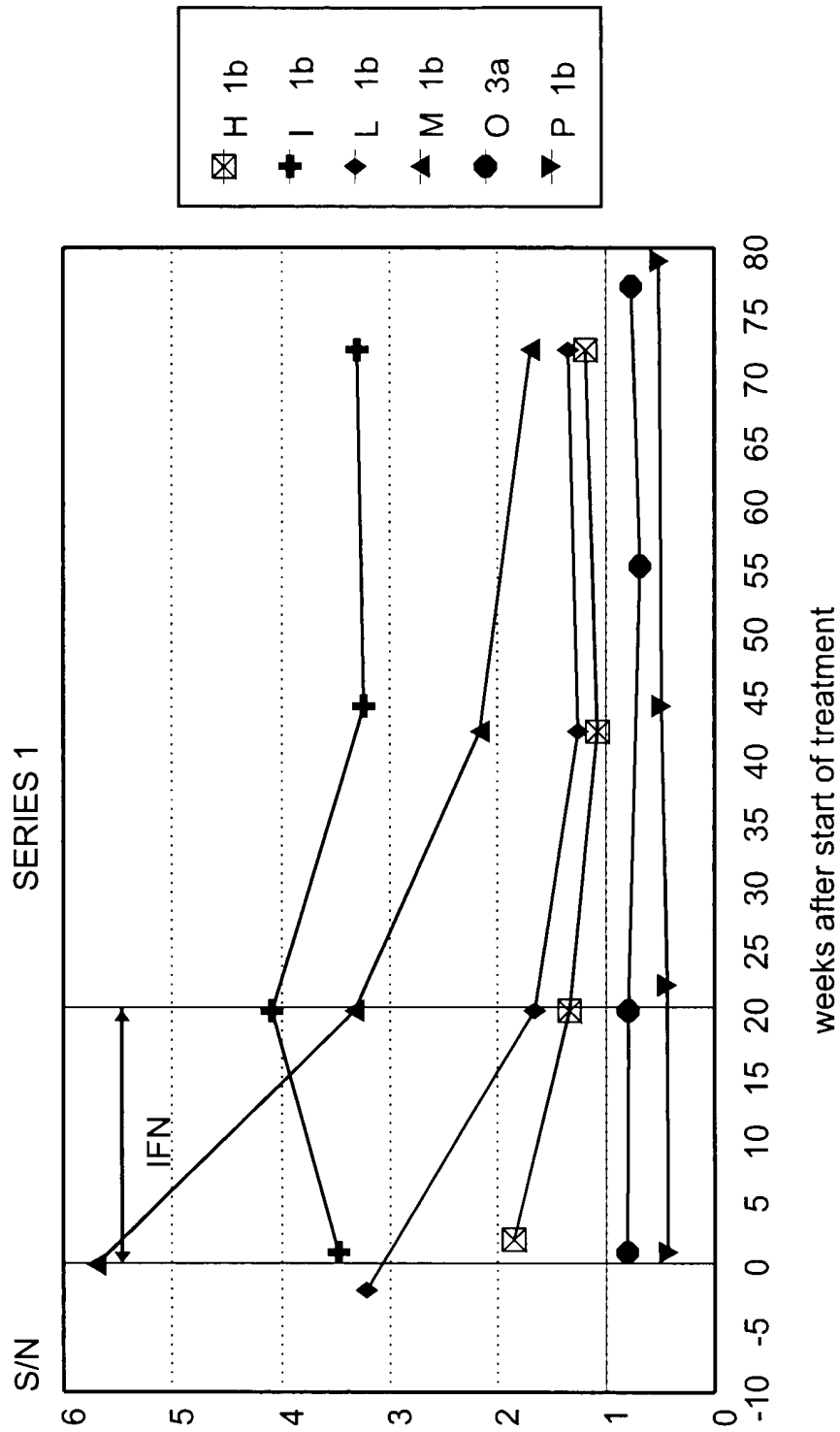


Figure 18

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 19 of 64
 Atty. Dkt.: 2551-69



Competition of reactivity of anti-E2 Mabs with peptides

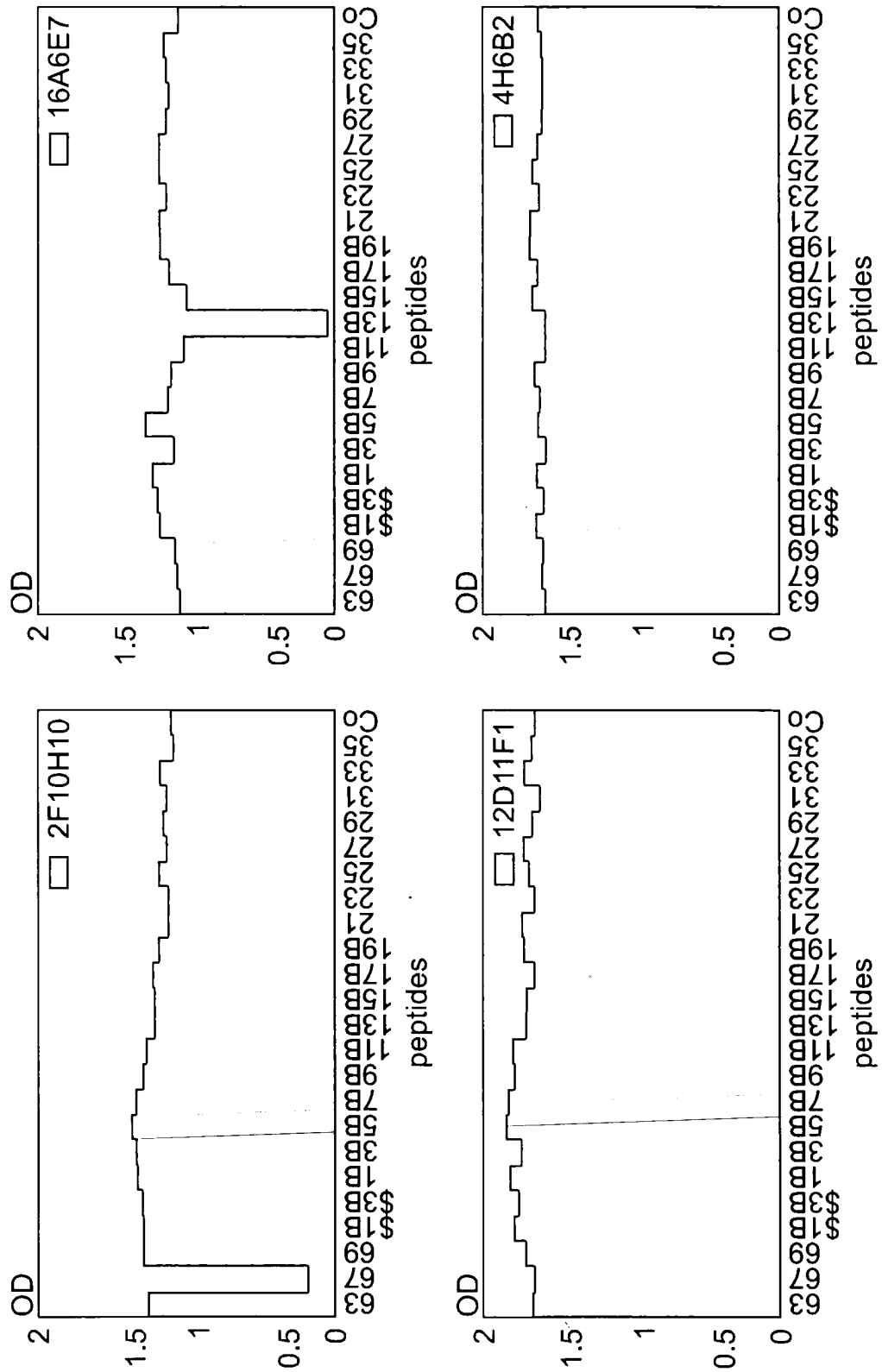


Figure 19

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 20 of 64
Atty. Dkt.: 2551-69



Human anti-E2 reactivity competed with peptides

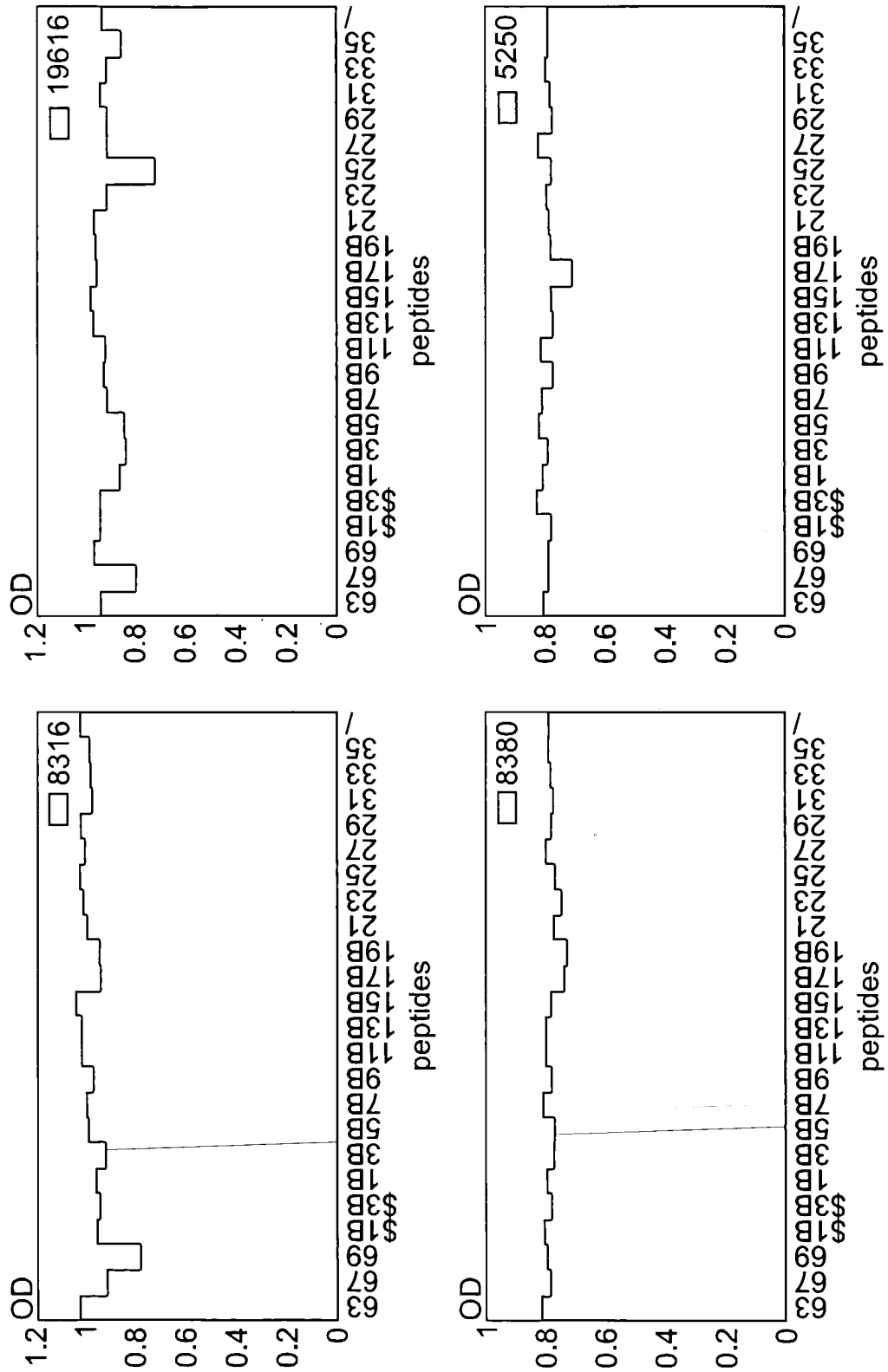


Figure 20



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 21 of 64
Atty. Dkt.: 2551-69

GGCATGCAAGCTTAATTAATT 3' (SEQ ID NO 1)
3' ACGTCCGTACGTTTCAATTAATTAATCGA 5' (SEQ ID NO 94)

5' CCGGGGAGGCCTGCACGTGATCGAGGGCAGACACCATCACCACCATCACTAATAGTTA
ATTAAGTCA 3' (SEQ ID NO 2)
3' CCTCCGGACGTGCACTAGCTCCCGTCTGTGGTAGTGGTGGTAGTGATTATCAATTAAT
TG 5' (SEQ ID NO 95)

SEQ ID NO 3 (HCC19A)
ATGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTACTGTCCTGTCTGACCATTCCA
GCTTCCGCTTATGAGGTGCGCAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCC
AACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCC
TGCGTTCCGGAGAACAACCTTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCT
AGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTGATTTGCTCGTTGGGGCG
GCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCC
CAGCTGTTACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATC
TATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAAGTGGTCGCCT
ACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG
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SEQ ID NO 5 (HCC110A)
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CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
TCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
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TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
ATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
GGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCAGCTGTTACCATCTCGCCTCGCCGG
CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCAACGT
ATGGCTTGGGATATGATGATGAAGTGGTCCCTACAACGGCCCTGGTGGTATCGCAGCTG
CTCCGGATCCCACAAGCTGTCTGTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCTTGGCG
GGTCTCGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTGATGCTACTC
TTTGCTCCCTAATAG

SEQ ID NO 7 (HCC111A)

Figure 21A



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 22 of 64
Atty. Dkt.: 2551-69

ATGTTGGGTAAGGTCATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATT
CCGCTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTT
CTGGAAGACGGCGTGAACATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTC
CTCTTGGCTTTACTGTCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTG
TCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACCTCTTCCCGC
TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACA
ATACGACGCCACGTGCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
GGGGATCTCTGCGGATCTGTCTTCCCTCGTCTCCAGCTGTTACCATCTCGCCTCGCCGG
CATGAGACGGTGCGAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTACCCGT
ATGGCTTGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 9 (HCC112A)

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GCTTCCGCTTATGAAGTGCACAACGTGTCCGGGGTGACCATGTCACGAACGACTGCTCC
AACTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCC
TGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCACGCTCGCGGCC
AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTGCGATTTGCTCGTTGGGGCT
GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTTGTTC
CAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC
TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCCTAA
TAG

SEQ ID NO 11 (HCC113A)

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AACTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCC
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AGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTGCGATTTGCTCGTTGGGGCT
GCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTTGTTC
CAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCAACTGCTCAATC
TATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 13 (HCC117A)

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CTGGAAGACGGCGTGAACATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTC
CTCTTGGCTTTACTGTCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGCAACGTG
TCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACCTCTTCCCGC
TGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAACGCCAGCATCCCCACTACAACA

Figure 21B

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 23 of 64
Atty. Dkt.: 2551-69



ATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
GGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTACCATCTCGCCTCGCCGG
CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTACCGT
ATGGCTTGGGATATGATGATGAACTGGTACTAATAG

SEQ ID NO 15 (HCP51)
ATGCCCCGTTGCTCTTTCTCTATCTT
SEQ ID NO 16 (HCP52)
ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCP53)
CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCP54)
CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCP107)
ATACGACGCCACGTCGATTCCCAGCTGTTACCATC

SEQ ID NO 20 (HCP108)
GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCC137)
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CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
TCCGGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACCTCTCCCGC
TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
ATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCGCCGGCATGAGACGGTG
CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTACCGTATGGCTTGGGAT
ATGATGATGAACTGGTGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCA
CAAGCTGTGCTGGACATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGGGTCTCGCCTAC
TATTCCATGGTGGGGAACGGGCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCCCTAA
TAG

SEQ ID NO 23 (HCC138)
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CTGGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGTTGCTCTTTCTCTATCTTC
CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
TCCGGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG

Figure 21C



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 24 of 64
Atty. Dkt.: 2551-69

GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACCTCTTCCCGC
TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
ATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCGCCGGCATGAGACGGTG
CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTACCGTATGGCTTGGGAT
ATGATGATGAACTGGTAATAG

SEQ ID NO 25 (HCC139)

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CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
TCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACCTCTTCCCGC
TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
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CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTACCGTATGGCTTGGGAT
ATGATGATGAACTGGTTCGCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCTC
TAATAG

SEQ ID NO 27 (HCC140)

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CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
TCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
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TGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
ATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCGCCGGCATGAGACGGTG
CAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTACCGTATGGCTTGGGAT
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ATCGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 29 (HCC162)

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CTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGCCCTT
GAAGACGGGATAAATTTGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTTTCTT
CTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGCGGAATACGTCT
GGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGCCGATGAC
GTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACATCCACGTGC
TGGACCCAGTGACACCTACAGTGGCAGTCAAGTACGTTCGGAGCAACCACCGCTTCGATA
CGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGCGCTCTACGTGGGT
GACATGTGTGGGGCTGTCTTCTCGTGGGACAAGCCTTCACGTTACAGACCTCGTCGCCAT

Figure 21D



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 25 of 64
Atty. Dkt.: 2551-69

CAAACGGTCCAGACCTGTAAGTCTCGCTGTACCCAGGCCATCTTTCAGGACATCGAATG
GCTTGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 31 (HCC163)

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GAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATT
CTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCTTACCGAAATGCCTCT
GGGATTTATCATGTTACCAATGATTGCCAAACTCTTCCATAGTCTATGAGGCAGATAAC
CTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCTATGACAGGTAATGTGAGTAGATGC
TGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCACGGCTCCTCTT
CGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCGTTATACGTAGGA
GACGCGTGTGGGGCACTATTCTTGTTAGGCCAAATGTTTACCTATAGGCCTCGCCAGCAC
GCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGTTACCGGCCACCGGATG
GCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCP109)

TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCP72)

CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

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GCCTACTATTCCATGGTGGGGAAGTGGGCTAAGTTTTGGTTGTGATGCTACTCTTTGCC
GGCGTCGACGGGCATACCCGCGTGTGAGGAGGGGAGCAGCCTCCGATACCAGGGGCCTT
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TGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCC
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CGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCTCACTTACACTGAGCCTAACAGC
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TCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACC
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AACAACACGCGGCCGCCGCGAGGCAACTGGTTCCGCTGTACATGGATGAATGGCACTGGG
TTCACCAAGACGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTTG
ACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCT
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TGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGG
TTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAGA
TCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCTTC

Figure 21E



Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 26 of 64
 Atty. Dkt.: 2551-69

ACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTG
 CAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTGCATCAAATGGGAGTATGTC
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 CTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTG
 GCCGGGGCGCATGGCACTCTTCTCCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAG
 GGCAGGCTGGTCCCTGGTGGGCATACGCCCTTCTATGGCGTGTGGCCGCTGCTCCTGCTT
 CTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA

SEQ ID NO 37 (HCC141)

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 CGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGC
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 TGTGTCCCTCTTTAGCCCCGGGTGGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAG
 TTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGC
 CGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTG
 TCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAG
 CTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGC
 GTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCGAGCCCTGTTGTGGTGGGGACGAC
 CGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCT
 CAACAACACGCGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGG
 GTTCACCAAGACGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTT
 GACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCT
 TGGGGCCTGGCTGACACCTAGGTGTATGGTTTCATTACCCATATAGGCTCTGGCACTACCC
 CTGCACTGTCAACTTCACCATCTTCAAGTTAGGATGTACGTGGGGGGCGTGGAGCACAG
 GTTCGAAGCCGCATGCAATTGGAAGTGGAGAGAGCGTTGTGACTTGGAGGACAGGGATAG
 ATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGAGTGGCAGAGCTTAATT
 AATTAG

SEQ ID NO 39 (HCC142)

GATCCCACAAGCTGTGCTGGACATGGTGGCGGGGGCCATTGGGGAGTCCTGGCGGGCCT
 CGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGC
 CGGCGTCGACGGGCATACCCGCGTGTGAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCT
 TGTGTCCCTCTTTAGCCCCGGGTGGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAG
 TTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGC
 CGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTG
 TCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAG
 CTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGC
 GTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCGAGCCCTGTTGTGGTGGGGACGAC
 CGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCT
 CAACAACACGCGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGG
 GTTCACCAAGACGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTT

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 27 of 64
Atty. Dkt.: 2551-69

GACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTC
TGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCC
CTGCACTGTCAACTTCACCATCTTCAAGTTAGGATGTACGTGGGGGGCGTGGAGCACAG
GTTTGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAG
ATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGGTGATCGAGGGCAGACACCATCACC
ACCATCACTAATAG

SEQ ID NO 41 (HCC143)

ATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGG
CATACCCGCGTGTGAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTT
AGCCCCGGGTGCGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAAC
AGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTAC
AAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTGCTCCATCGAC
AAGTTCGCTCAGGGGTGGGGTCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG
CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGC
GGTCCAGTGTATTGCTTACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTTTGGT
GTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG
CCGCCGCGAGGCAACTGGTTGCGCTGTACATGGATGAATGGCACTGGGTTTACCAAGACG
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GACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTG
ACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAAC
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TGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGC
CCGCTGCTGCTGTCTACAACAGAGTGGCAGAGCTTAATTAATTAG

SEQ ID NO 43 (HCC144)

ATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGG
CATACCCGCGTGTGAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTT
AGCCCCGGGTGCGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAAC
AGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTAC
AAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTGCTCCATCGAC
AAGTTCGCTCAGGGGTGGGGTCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG
CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGC
GGTCCAGTGTATTGCTTACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTTTGGT
GTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG
CCGCCGCGAGGCAACTGGTTGCGCTGTACATGGATGAATGGCACTGGGTTTACCAAGACG
TGTGGGGGGCCCCCGTGCACATCGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACT
GACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTG
ACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAAC
TTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGGTTTGAAGCCGCA
TGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGC

Figure 21G



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 28 of 64
Atty. Dkt.: 2551-69

CGCTGCTGCTGTCTACAACAGGTGATCGAGGGCAGACACCATCACCACCATCACTAATA

SEQ ID NO 45 (HCCL64)

ATGGTGGCGGGGGCCCATTTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGG
AACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGC
GTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGG
TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCC
CTGAAC TGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAAA
TTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTGCTCCATCGACAAGTTCGCT
CAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGGCCCTACTGC
TGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTG
TATTGCTTACCCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACG
TATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAACACGCGGCCCGCCGCGA
GGCAACTGGTTCCGGCTGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGGC
CCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTT
CGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGG
TGTATGGTTCAATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATC
TTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGG
ACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTG
CTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCCCTTACCACCCTGCCGGCCCTATCC
ACCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGGG
TCGGCGGTTGTCTCCCTTGTATCAAATGGGAGTATGTCCTGTTGCTCTTCTTCTCCTG
GCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCC
GCCTTAGAGAACCTGGTGGTCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTT
TCCTTCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGGC
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GCTTATGCCTAGTAA

SEQ ID NO 47 (HCC165)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATT
CCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT
CTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTC
CTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTG
TCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCG
GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAACAACCTTTCCCGC
TGCTGGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACA
ATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
GGGGACCTCTGCGGATCTGTCTTCTCGTCTCCAGCTGTTACCATCTCGCCTCGCCGG
CATGAGACGGTGACGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTACACGT
ATGGCTTGGGATATGATGATGAACTGGTCGCTACAACGGCCCTGGTGGTATCGCAGCTG
CTCCGGATCCCACAAGCTGTGCTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCTTGGCG

Figure 21H



Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 29 of 64
 Atty. Dkt.: 2551-69

GGCCTCGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTC
 TTTGCCGGCGTCGACGGGCATACCCGCGTGTGAGGAGGGGCAGC AGCCTCCGATACCAG
 GGGCCTTGTGTCCCTCTTTAGCCCCGGGTGCGCTCAGAAAATCCAGCTCGTAAACACCAA
 CGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTT
 CTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGC
 CAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCTCACTTACACTGAGCC
 TAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGT
 ACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTACCCCGAGCCCTGTTGTGGTGGG
 GACGACCGATCGGTTTTGGTGTCCCCACGTATAACTGGGGGGCGAAGCACTCGGATGTGCT
 GATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGG
 CACTGGGTTACCAAGACGTGTGGGGGCCCCCGTGAACATCGGGGGGGCCGGCAACAA
 CACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATG
 CGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCA
 CTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGA
 GCACAGGTTGGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAG
 GGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTG
 TTCCTTACCAACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAACATCGT
 GGACGTGCAATACCTGTACGGTGTAGGGTGGCGGTTGTCTCCCTTGTATCAAATGGGA
 GTATGTCCTGTTGCTCTTCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGCTTATGGAT
 GATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCTCAATGCGGC
 GGCGGTGGCCGGGGCGCATGGCACTCTTCTTCTTGTGTTCTTCTGTGCTGCCTGGTA
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SEQ ID NO 49 (HCC166)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAG
 GACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGG
 GGCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCAACCTCGTGGG
 AGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGGCTCAGCCGGG
 TACCCTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCC
 CGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCGGCGTAGGTGCGCTAATTTGGGT
 AAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCGCTCGTC
 GGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGAC
 GGCGTGAACCTATGCAACAGGGAATTTGCCGGTTGCTCTTCTCTATCTTCTTGGCT
 TTGCTGTCTGTGCTGACCGTTCCAGCTTCCGCTTATGAAGTGCAGCAACGTGTCCGGGATG
 TACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATGAGGCAGCGGACATGATC
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 GCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGC
 CACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGACCTC
 TGCGGATCTGTCTTCTCGTCTCCAGCTGTTACCATCTCGCTCGCCGGCATGAGACG
 GTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATGGCTTGG

Figure 211



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 30 of 64
Atty. Dkt.: 2551-69

ATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATC
CCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCCTGGCGGGCCTCGCC
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GTCGACGGGCATACCCGCGTGTGAGGAGGGGAGCAGCCTCCGATACCAGGGGCCTTGTG
TCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGG
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CTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTCGC
TCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCTCACTTAACTGAGCCTAACAGCTCG
GACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCT
CAGGTGTGCGGTCCAGTGTATTGCTTACCCCCGAGCCCTGTTGTGGTGGGGACGACCGAT
CGGTTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAAC
AACACGCGGCCGCCGCGAGGCAACTGGTTCCGGCTGTACATGGATGAATGGCACTGGGTTC
ACCAAGACGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTTGACC
TGCCCCACTGACTGTTTTTCGGAAGCACCCGAGGCCACCTACGCCAGATGCGGTTCTGGG
CCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCCCTGC
ACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGGTTG
GAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCA
GAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCCCTTACC
ACCCTGCCGGCCCTATCCACCGGCCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAA
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TTGCTCTTCCCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTG
ATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGGCGGCCGTGGCC
GGGGCGCATGGCACTCTTTCCCTTCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGC
AGGCTGGTCCCTGGTGGGCATACGCCTTCTATGGCGTGTGGCCGCTGCTCCTGCTTCTG
CTGGCCTTACCACCACGAGCTTATGCCTAGTAA

Figure 21J



Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 31 of 64
 Atty. Dkt.: 2551-69

OD measured at 450nm
 construct

| Fraction | Volume | dilution | 39 type 1b | 40 type 1b | 62 type 3a | 63 type 5a |
|--------------|--------|----------|---------------|---------------|---------------|---------------|
| Start | 23ml | 1/20 | 2.517 | 1.954 | 1.426 | 1.142 |
| Flow through | 23ml | 1/20 | 0.087 | 0.085 | 0.176 | 0.120 |
| 1 | 0.4ml | 1/200 | 0.102 | 0.051 | 0.048 | 0.050 |
| 2 | | | 0.396 | 0.550 | 0.090 | 0.067 |
| 3 | | | 2.627 | 2.603 | 2.481 | 2.372 |
| 4 | | | 3 | 2.967 | 3 | 2.694 |
| 5 | | | 3 | 2.810 | 2.640 | 2.154 |
| 6 | | | 2.694 | 2.499 | 1.359 | 1.561 |
| 7 | | | 2.408 | 2.481 | 0.347 | 1.390 |
| 8 | | | 2.176 | 1.970 | 1.624 | 0.865 |
| 9 | | | 1.461 | 1.422 | 0.887 | 0.604 |
| 10 | | | 1.286 | 0.926 | 0.543 | 0.519 |
| 11 | | | 0.981 | 0.781 | 0.294 | 0.294 |
| 12 | | | 0.812 | 0.650 | 0.249 | 0.199 |
| 13 | | | 0.373 | 0.432 | 0.239 | 0.209 |
| 14 | | | 0.653 | 0.371 | 0.145 | 0.184 |
| 15 | | | 0.441 | 0.348 | 0.151 | 0.151 |
| 16 | | | 0.321 | 0.374 | 0.098 | 0.106 |
| 17 | | | 0.525 | 0.186 | 0.099 | 0.108 |
| 18 | | | 0.351 | 0.171 | 0.083 | 0.090 |
| 19 | | | 0.192 | 0.164 | 0.084 | 0.087 |

Figure 22



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 32 of 64
Atty. Dkt.: 2551-69

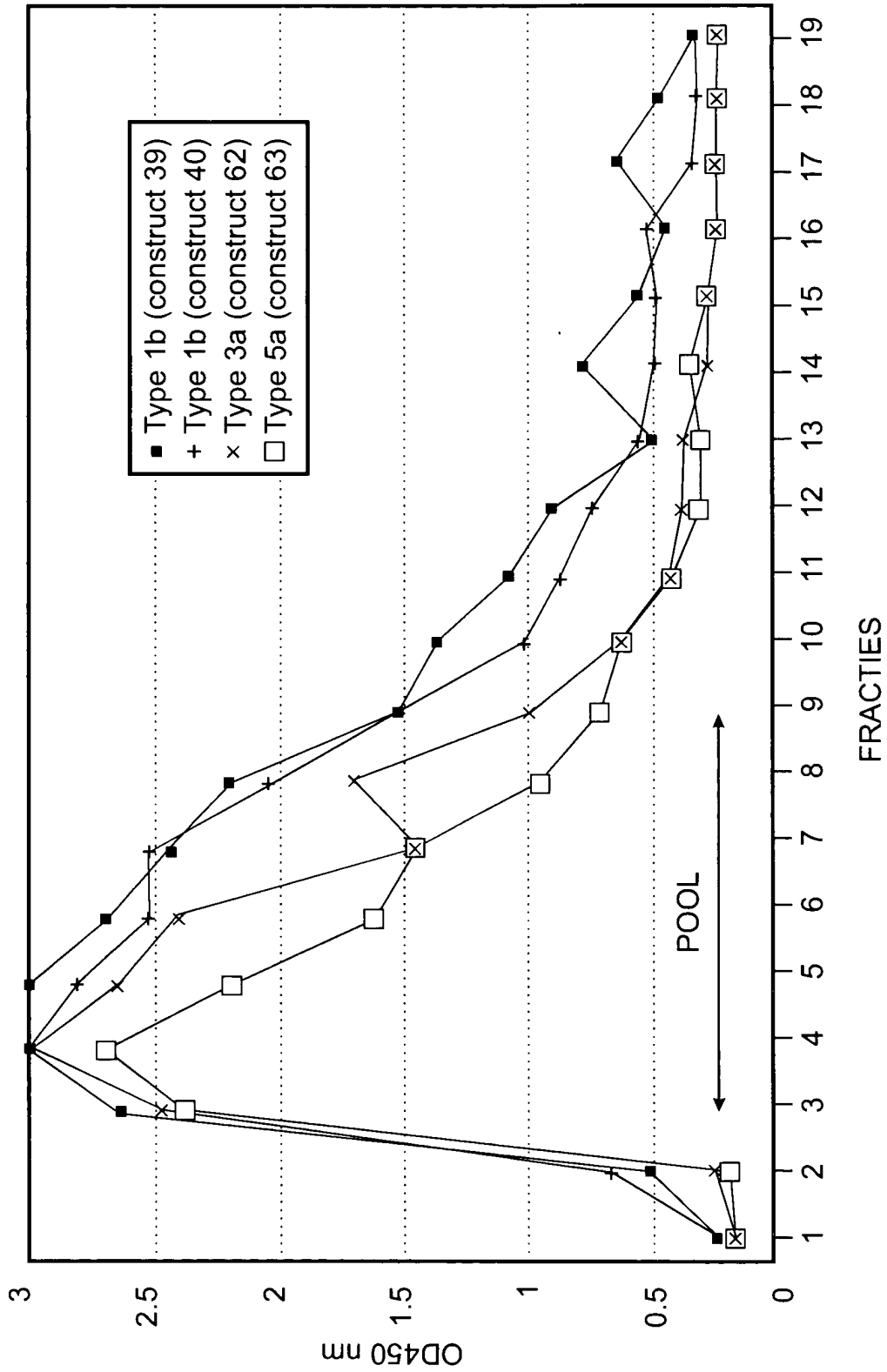


Figure 23



Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 33 of 64
 Atty. Dkt.: 2551-69

OD measured at 450nm
 construct

| Fraction | Volume | dilution | 39 type 1b | 40 type 1b | 62 type 3a | 63 type 5a |
|----------|--------|----------|---------------|---------------|---------------|---------------|
| 20 | 250µl | 1/200 | 0.072 | 0.130 | 0.096 | 0.051 |
| 21 | | | 0.109 | 0.293 | 0.084 | 0.052 |
| 22 | | | 0.279 | 0.249 | 0.172 | 0.052 |
| 23 | | | 0.093 | 0.151 | 0.297 | 0.054 |
| 24 | | | 0.080 | 0.266 | 0.438 | 0.056 |
| 25 | | | 0.251 | 0.100 | 0.457 | 0.048 |
| 26 | | | 3 | 1.649 | 0.722 | 0.066 |
| 27 | | | 3 | 3 | 2.528 | 0.889 |
| 28 | | | 3 | 3 | 3 | 2.345 |
| 29 | | | 3 | 3 | 2.849 | 2.580 |
| 30 | | | 2.227 | 1.921 | 1.424 | 1.333 |
| 31 | | | 0.263 | 0.415 | 0.356 | 0.162 |
| 32 | | | 0.071 | 0.172 | 0.154 | 0.064 |
| 33 | | | 0.103 | 0.054 | 0.096 | 0.057 |
| 34 | | | 0.045 | 0.045 | 0.044 | 0.051 |
| 35 | | | 0.043 | 0.047 | 0.045 | 0.046 |
| 36 | | | 0.045 | 0.045 | 0.049 | 0.040 |
| 37 | | | 0.045 | 0.047 | 0.046 | 0.048 |
| 38 | | | 0.046 | 0.048 | 0.047 | 0.057 |
| 39 | | | 0.045 | 0.048 | 0.050 | 0.057 |
| 40 | | | 0.046 | 0.049 | 0.048 | 0.049 |

Figure 24



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 34 of 64
Atty. Dkt.: 2551-69

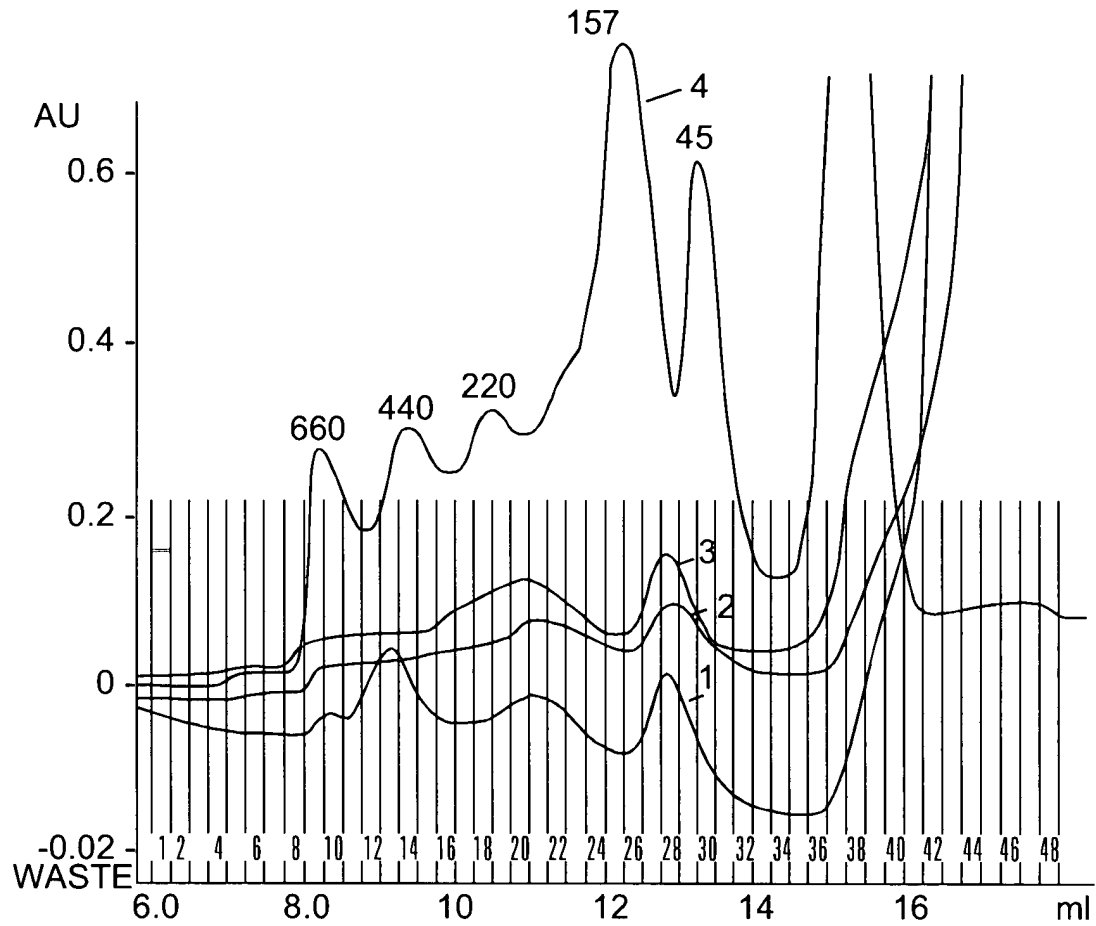


Figure 25

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 35 of 64
Atty. Dkt.: 2551-69

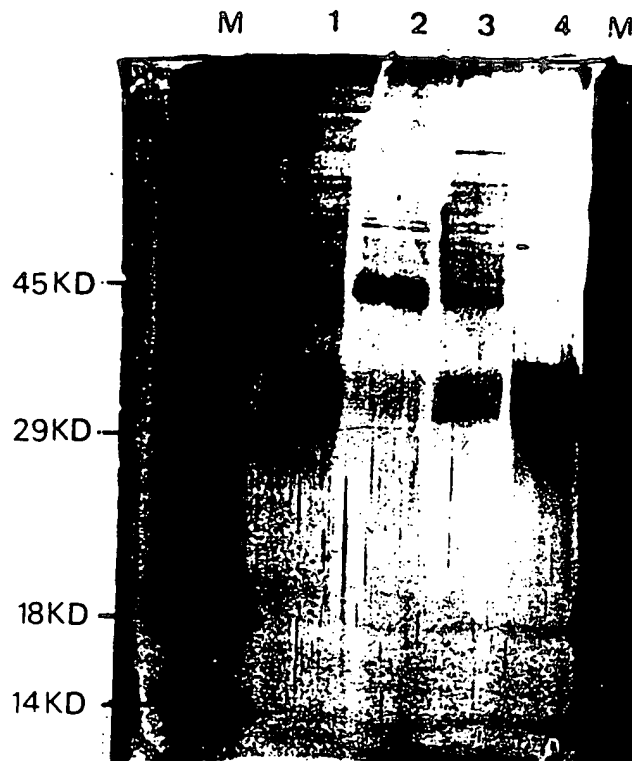


Fig. 26

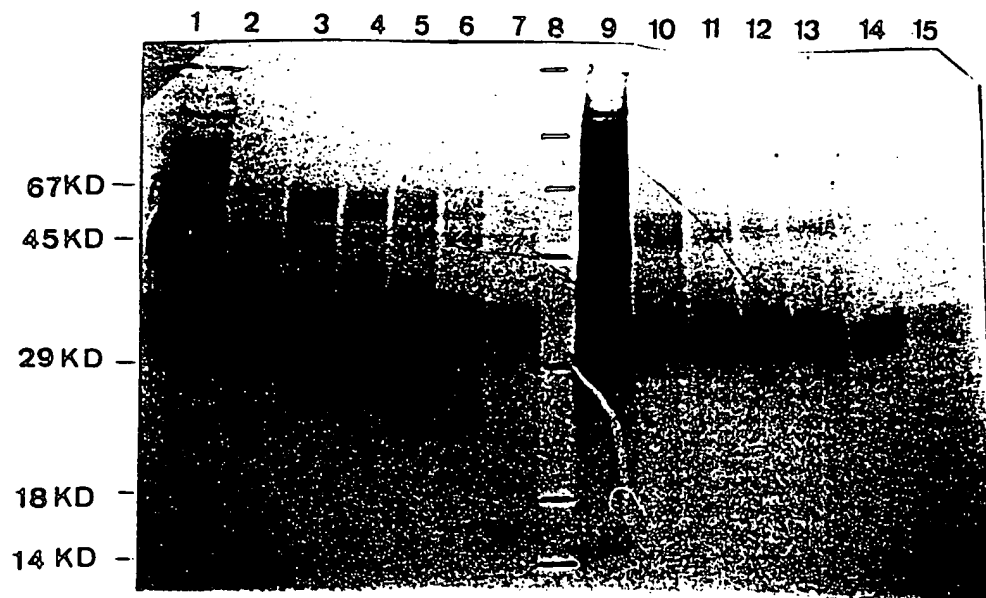


Fig. 27

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 36 of 64
 Atty. Dkt.: 2551-69

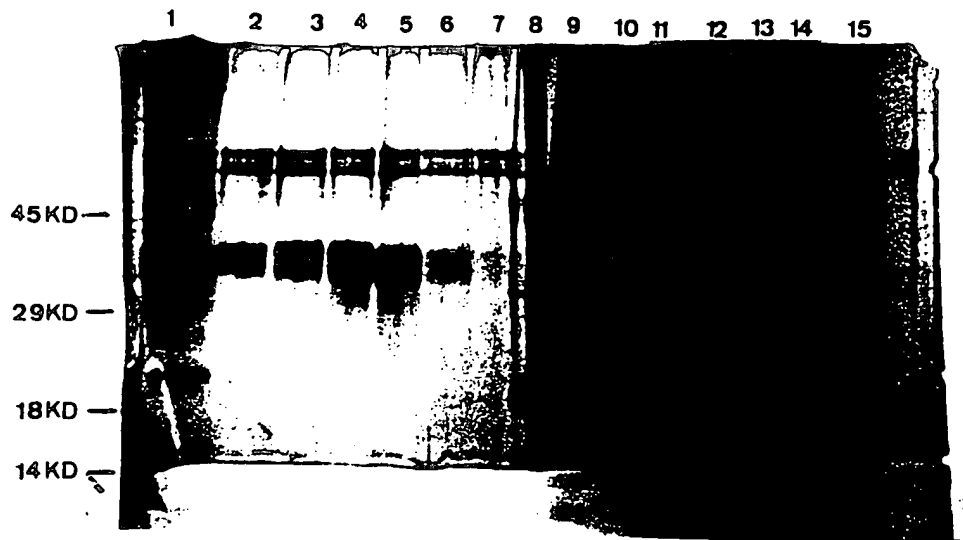


Fig.28

M 1 2 3 4 5 6

Fig.29

67 kD -

45 kD -

29 kD -

18 kD -

14 kD -

Lane 1: Crude Lysate
 Lane 2: Flow through Lentil Chromatography
 Lane 3: Wash with EMPIGEN Lentil Chromatography
 Lane 4: Eluate Lentil Chromatography
 Lane 5: Flow through during concentration lentil eluate
 Lane 6: Pool of E1 after Size Exclusion Chromatography

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 37 of 64
Atty. Dkt.: 2551-69

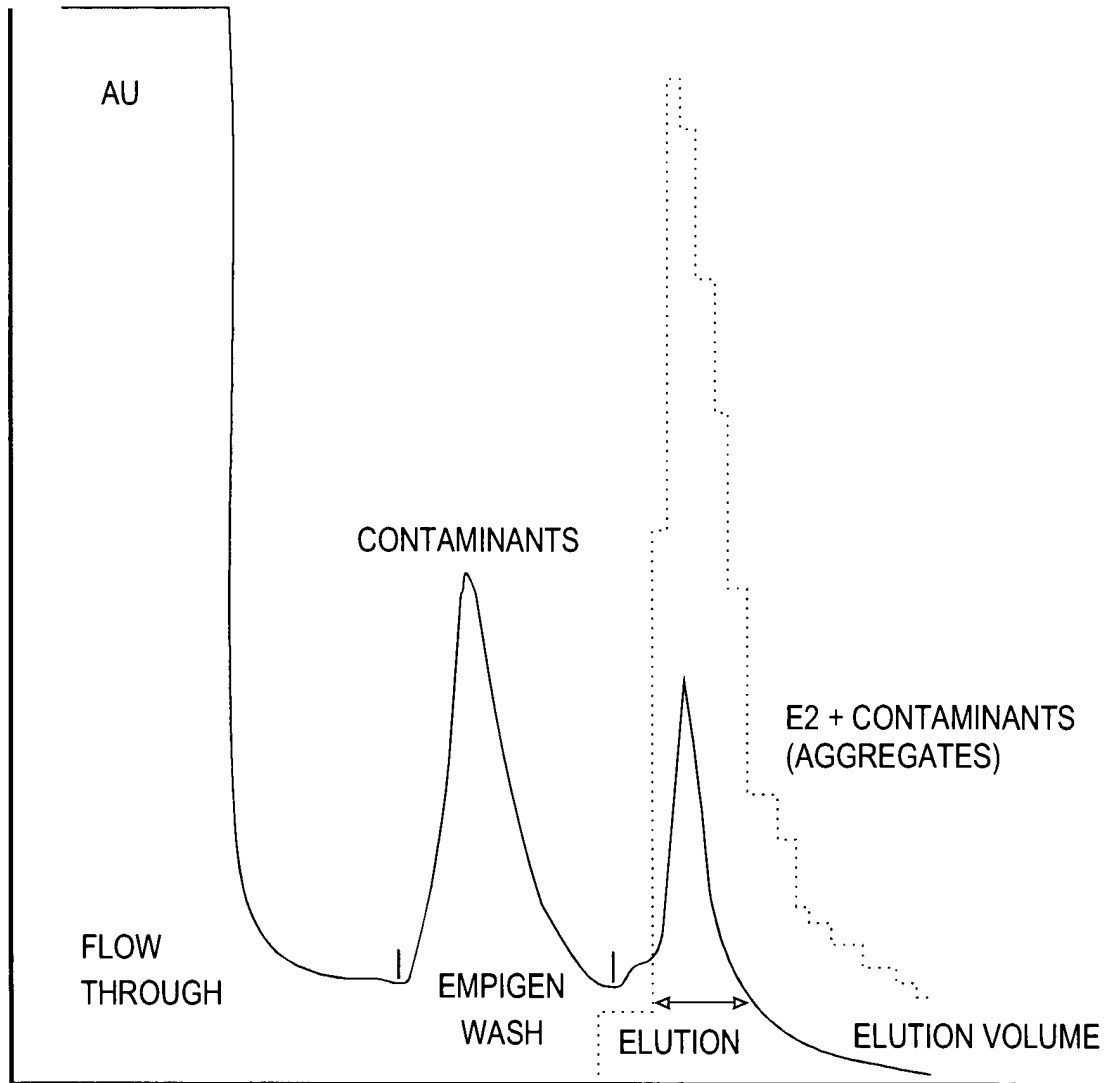


Figure 30

NON-REDUCED

38 / 65

E2 + CONTAMINANTS (AGGREGATES)

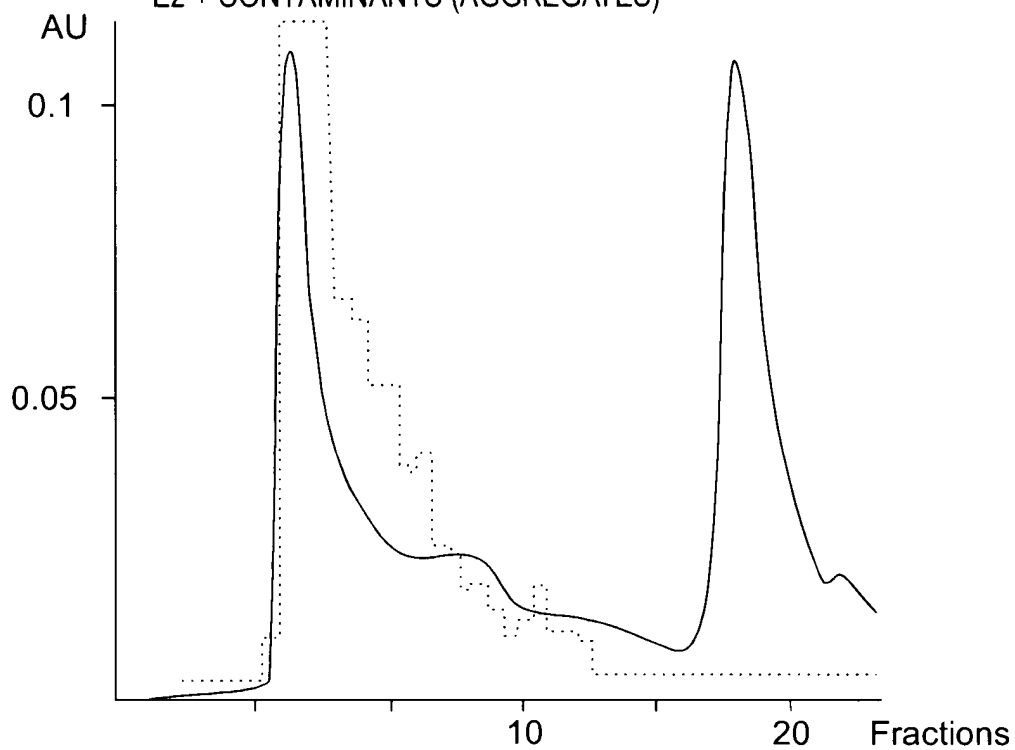


Figure 31A

REDUCED

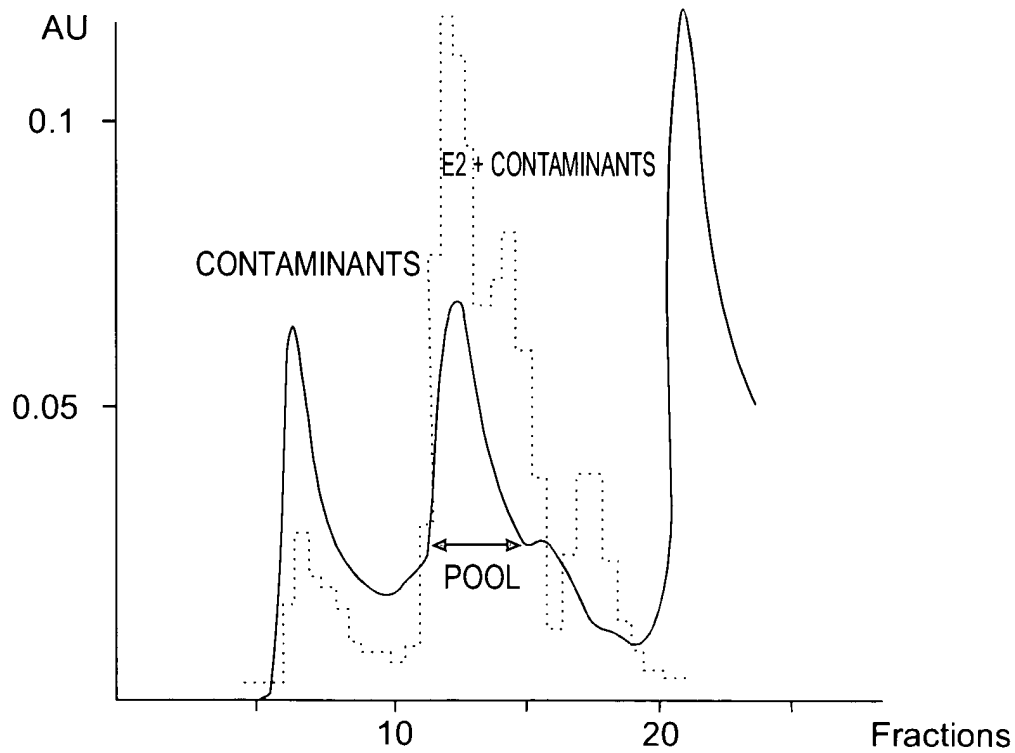
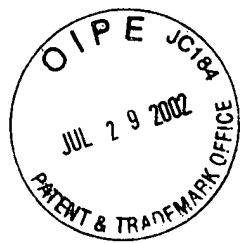


Figure 31B



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 39 of 64
Atty. Dkt.: 2551-69

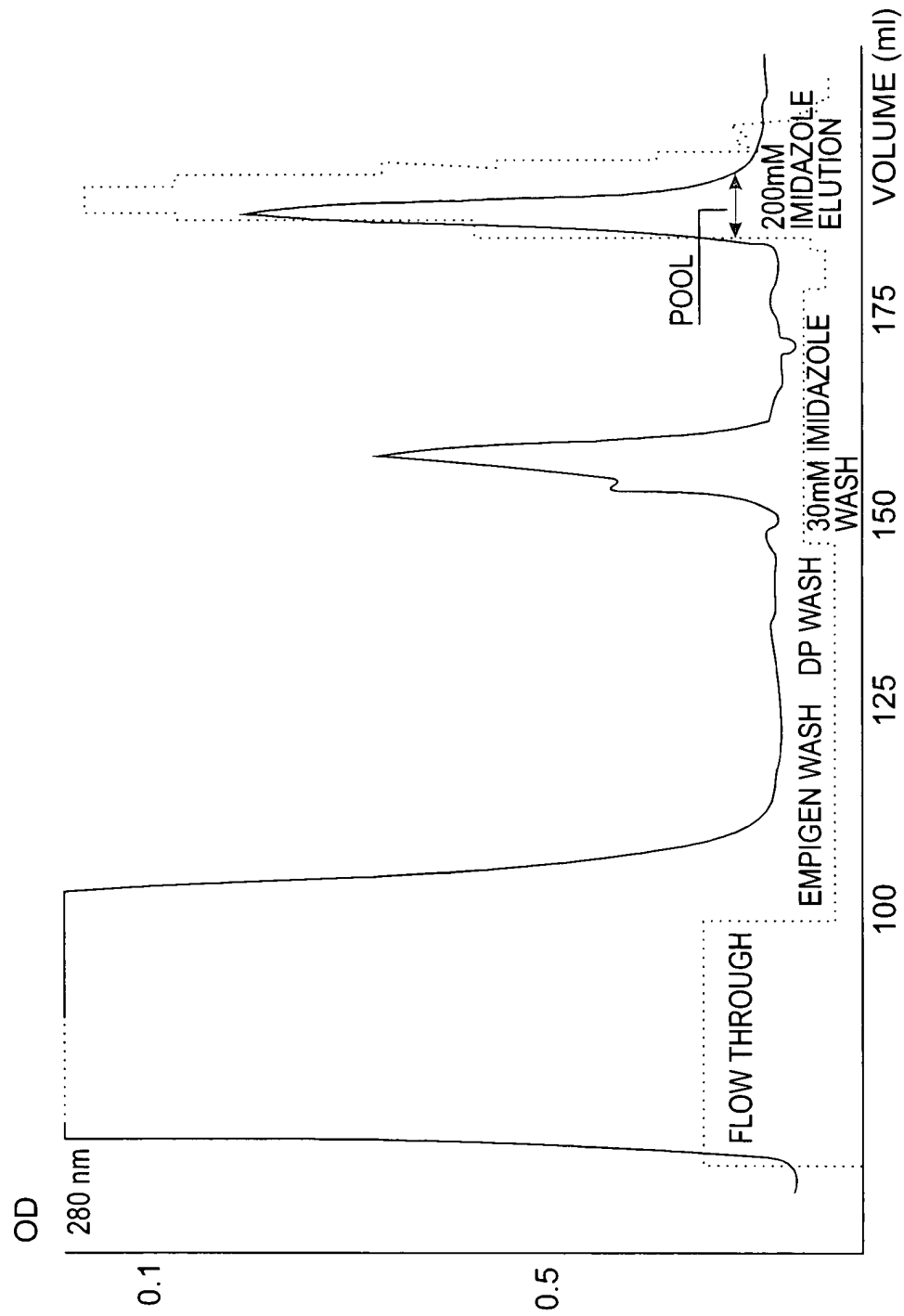
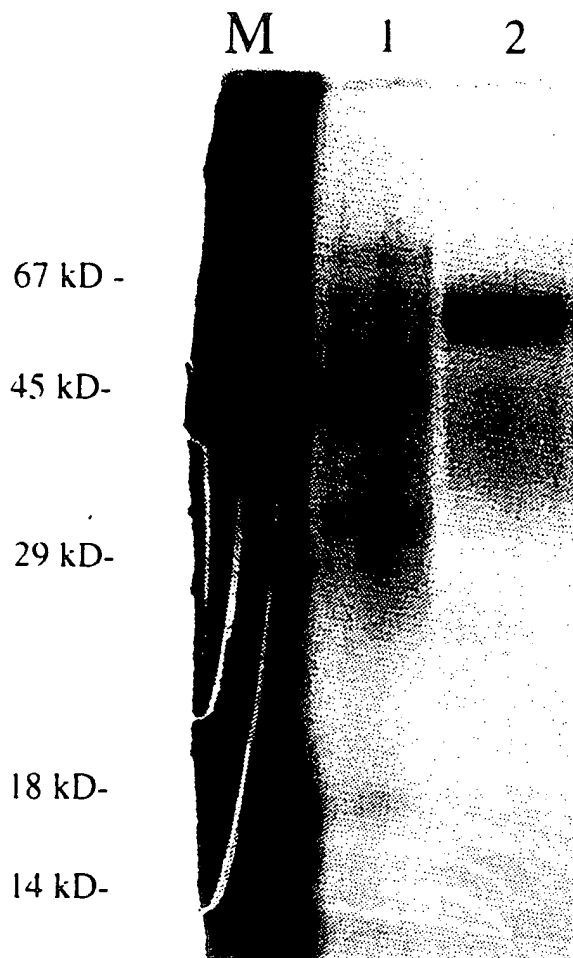


Figure 32

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 40 of 64
Atty. Dkt.: 2551-69



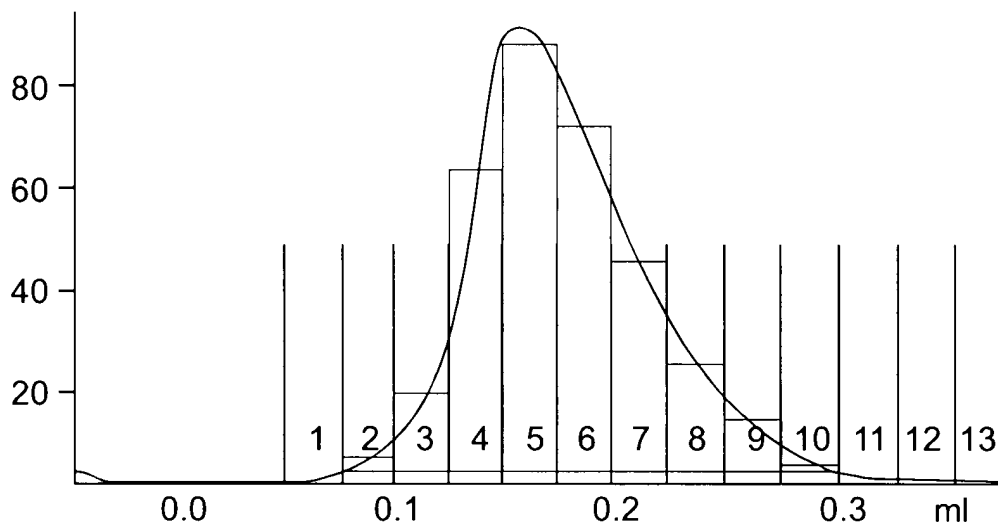
SILVER STAIN OF PURIFIED E2



1. 30 mM IMIDAZOLE WASH Ni-IMAC
2. 0.5 ug E2

Fig.33

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 41 of 64
 Atty. Dkt.: 2551-69



| No. | Ret (ml) | Peak start (ml) | Peak end (ml) | Dur (ml) | Area (ml*mAU) | Height (mAU) |
|-----|-------------|--------------------|------------------|-------------|------------------|-----------------|
| 1 | -0.45 | -0.46 | -0.43 | 0.04 | 0.0976 | 4.579 |
| 2 | 1.55 | 0.75 | 3.26 | 2.51 | 796.4167 | 889.377 |
| 3 | 3.27 | 3.26 | 3.31 | 0.05 | 0.0067 | 0.224 |
| 4 | 3.33 | 3.32 | 3.33 | 0.02 | 0.0002 | 0.018 |

Total number of detected peaks = 4

Total Area above baseline = 0.796522 ml*AU

Total area in evaluated peaks = 0.796521 ml*AU

Ratio peak area / total area = 0.999999

Total peak duration = 2.613583 ml

Figure 34

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 42 of 64
 Atty. Dkt.: 2551-69

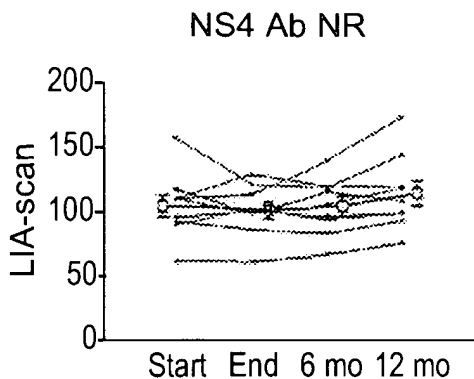


Fig. 35A-1

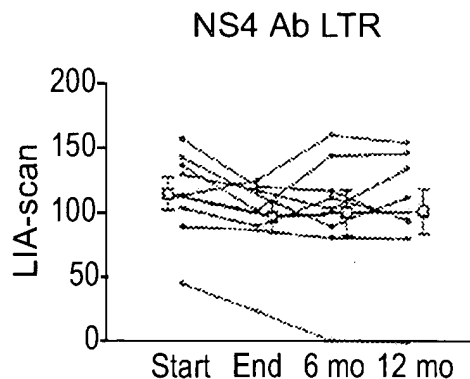


Fig. 35A-2

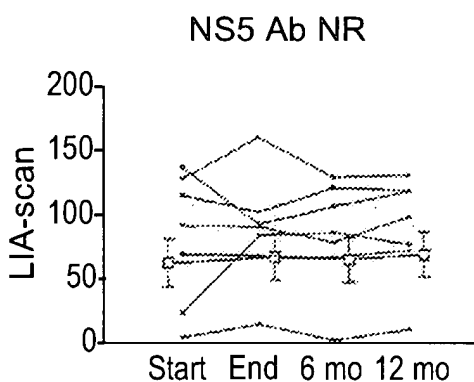


Fig. 35A-3

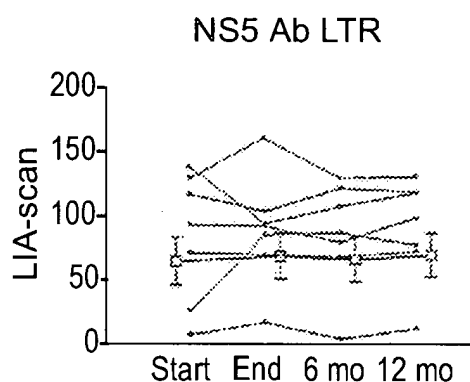


Fig. 35A-4

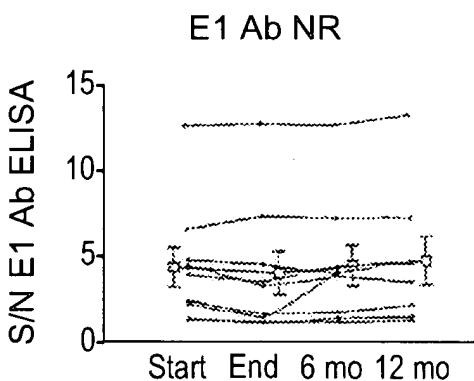


Fig. 35A-5

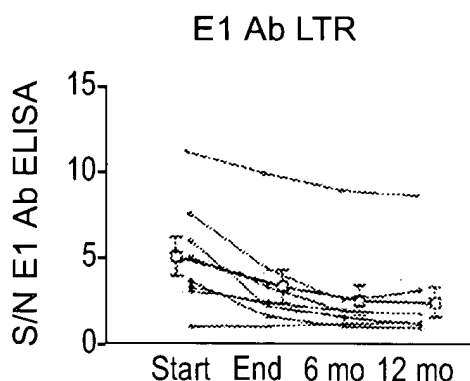


Fig. 35A-6

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 43 of 64
Atty. Dkt.: 2551-69

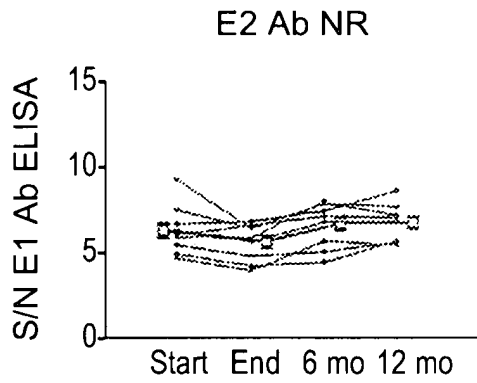
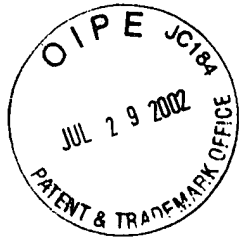


Fig. 35A-7

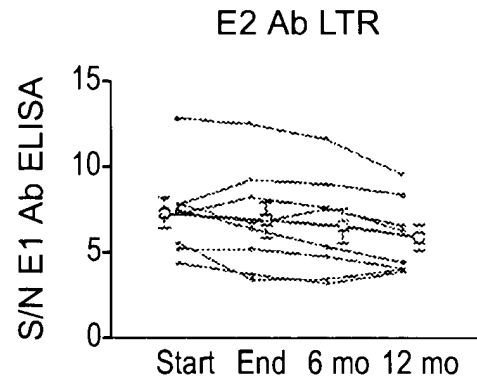


Fig. 35A-8

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 44 of 64
Atty. Dkt.: 2551-69

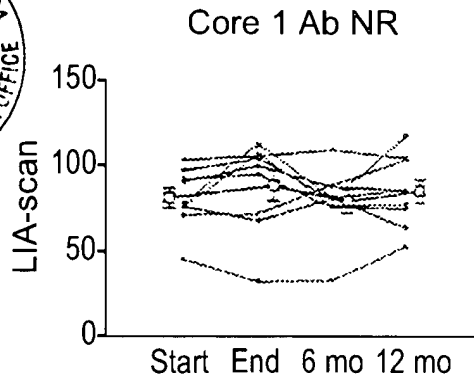


Fig. 35B-1

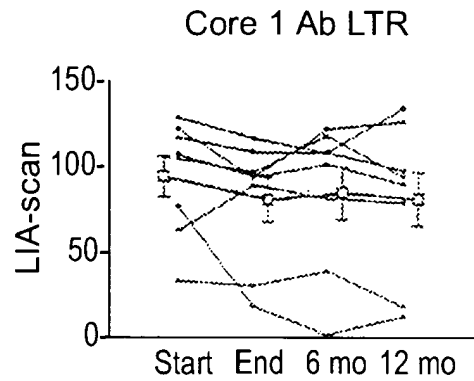


Fig. 35B-2

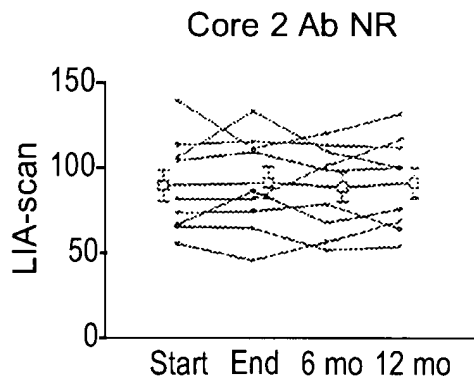


Fig. 35B-3

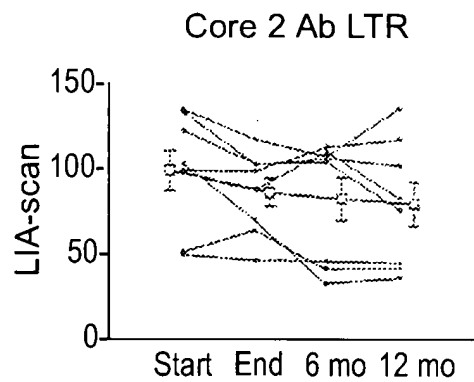


Fig. 35B-4

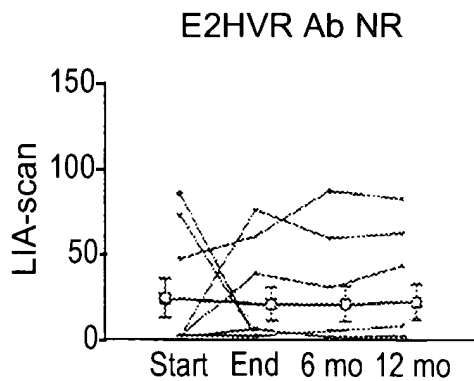


Fig. 35B-5

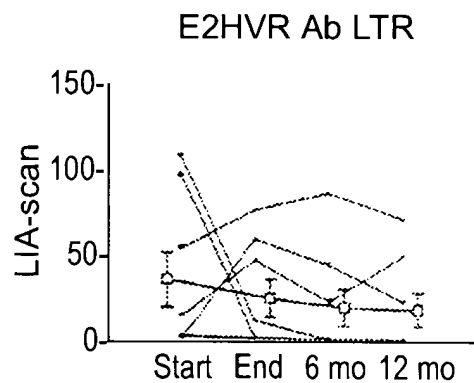


Fig. 35B-6

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 45 of 64
Atty. Dkt.: 2551-69

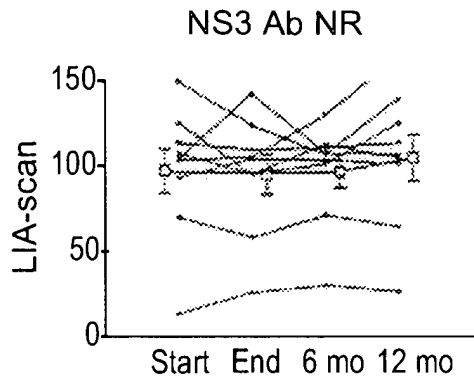


Fig. 35B-7

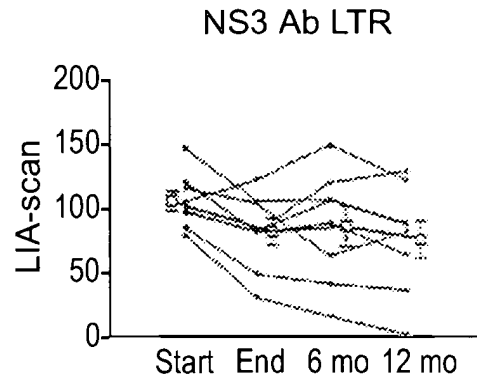


Fig. 35B-8

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 46 of 64
Atty. Dkt.: 2551-69

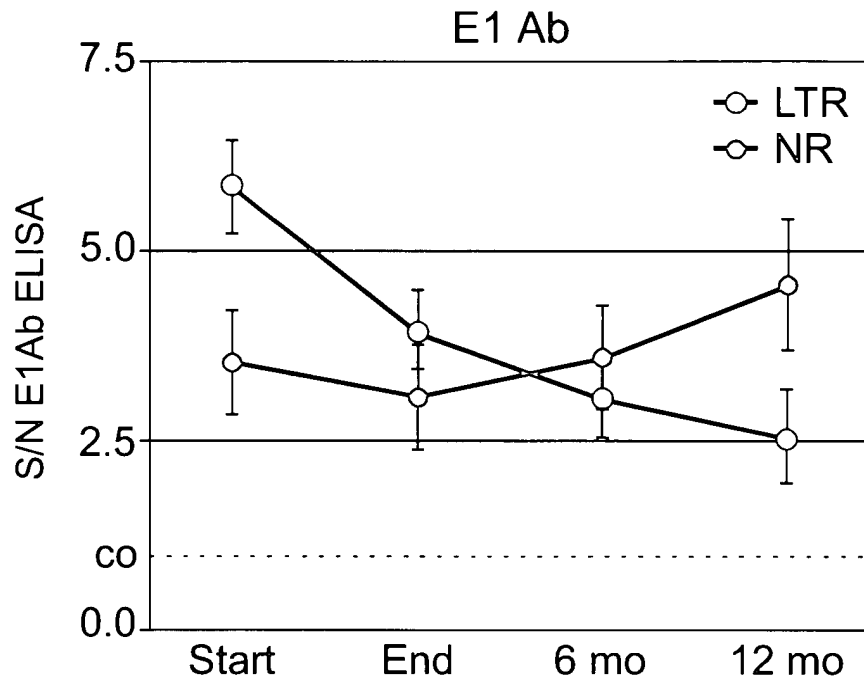
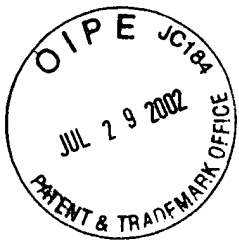


Figure 36A

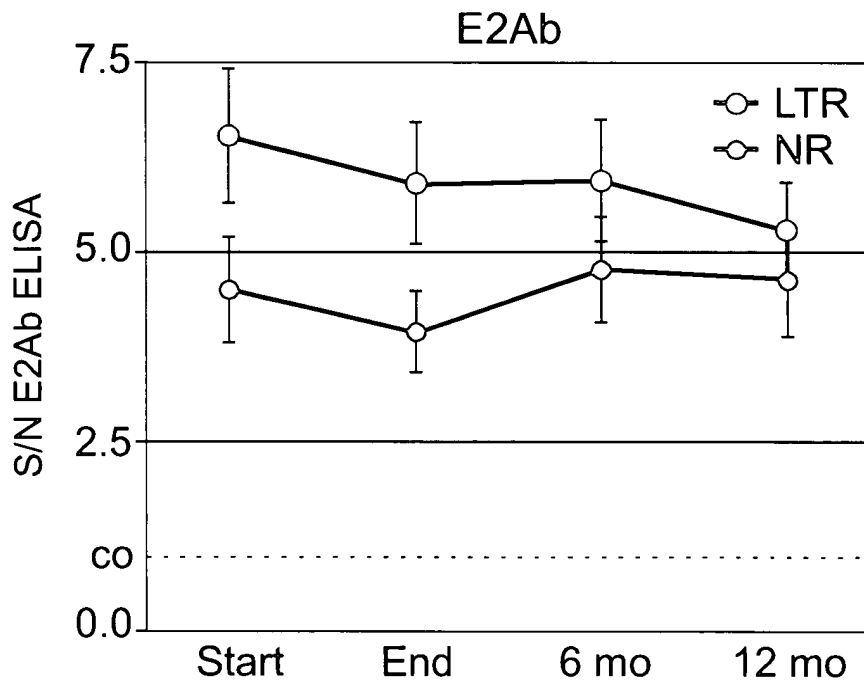


Figure 36B

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 47 of 64
Atty. Dkt.: 2551-69

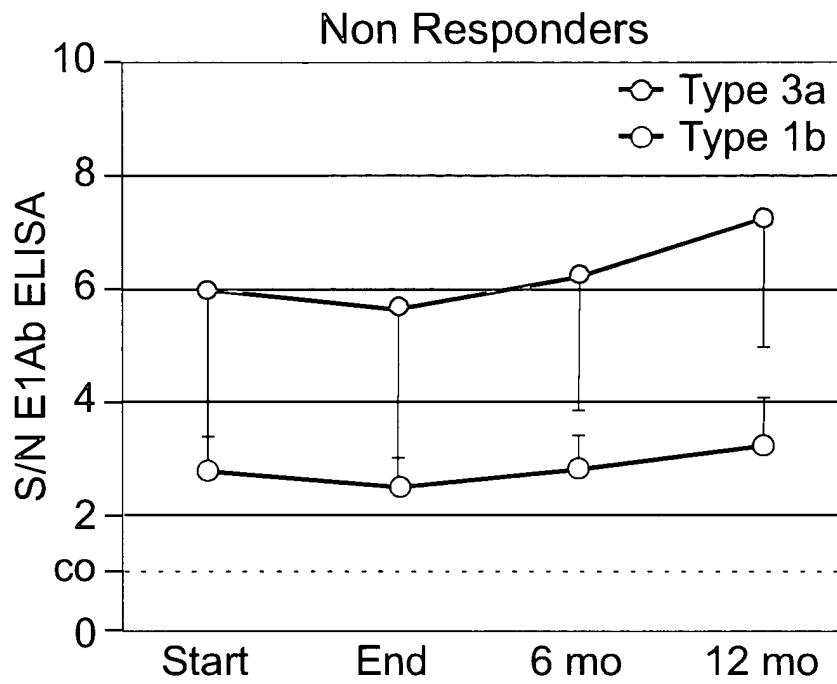


Figure 37A

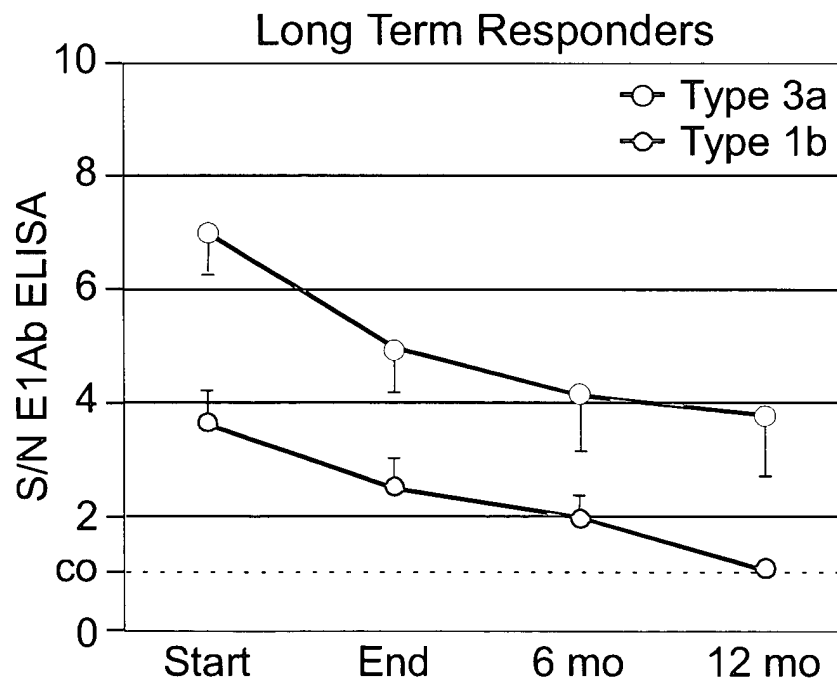


Figure 37B



Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 48 of 64
Atty. Dkt.: 2551-69

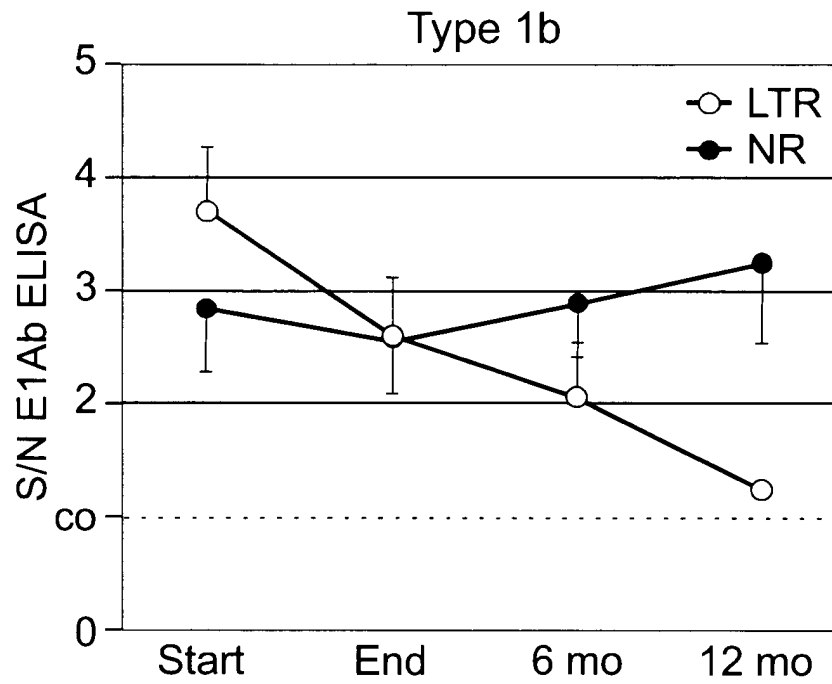


Figure 37C

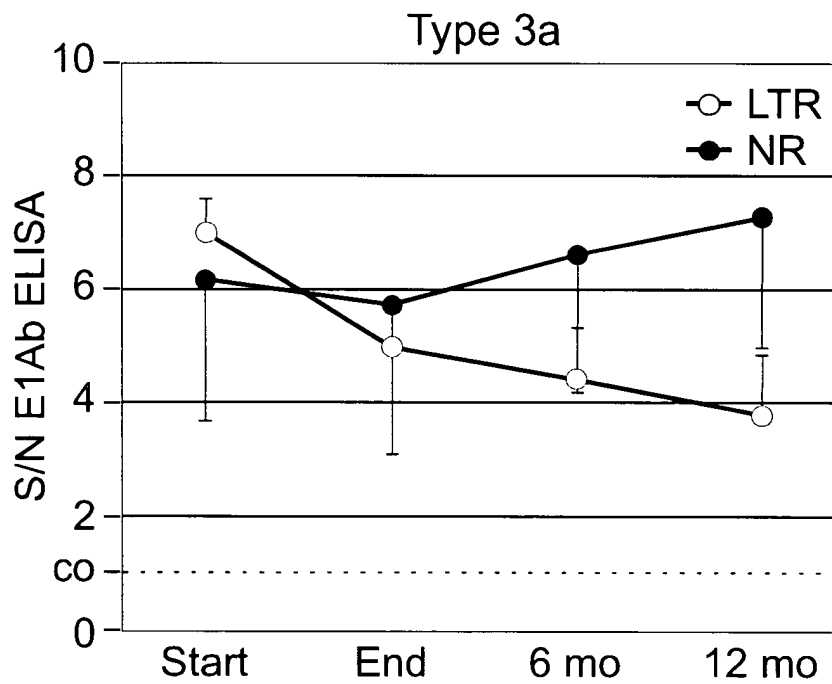


Figure 37D

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 49 of 64
Atty. Dkt.: 2551-69



Relative Map Positions of
anti-E2 monoclonal antibodies

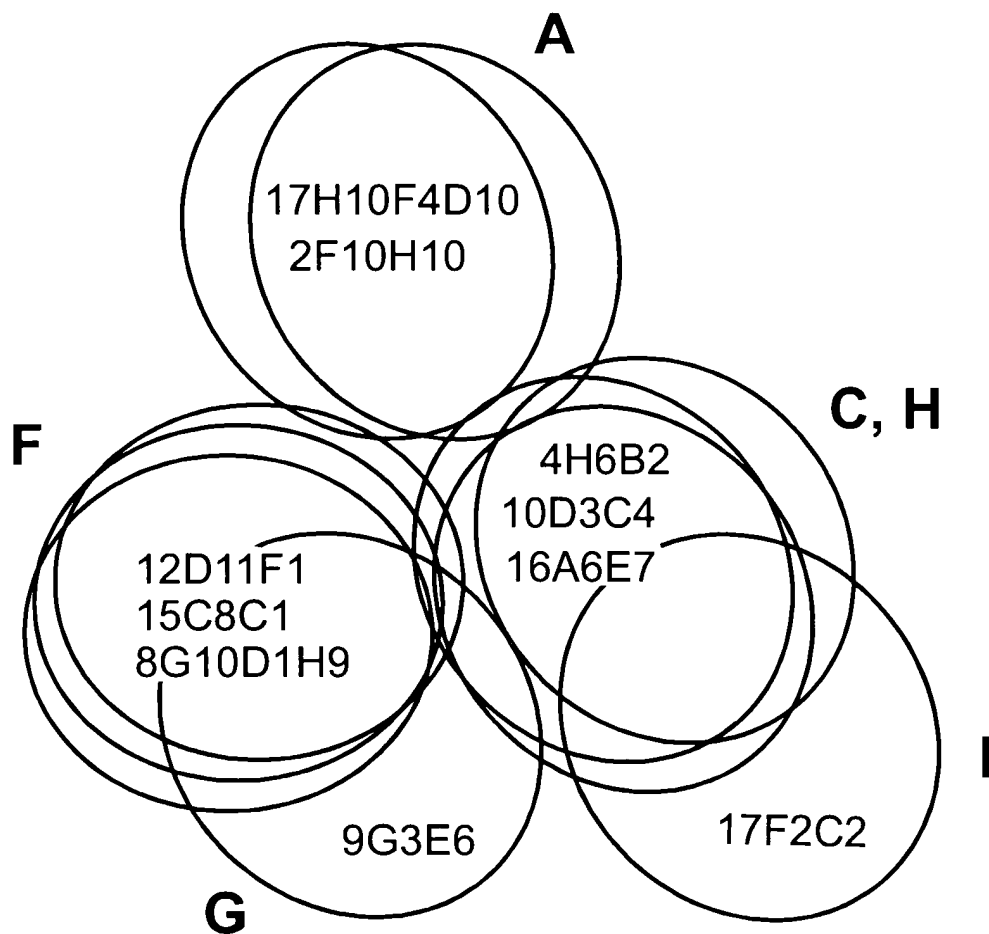


Figure 38

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 50 of 64
 Atty. Dkt.: 2551-69

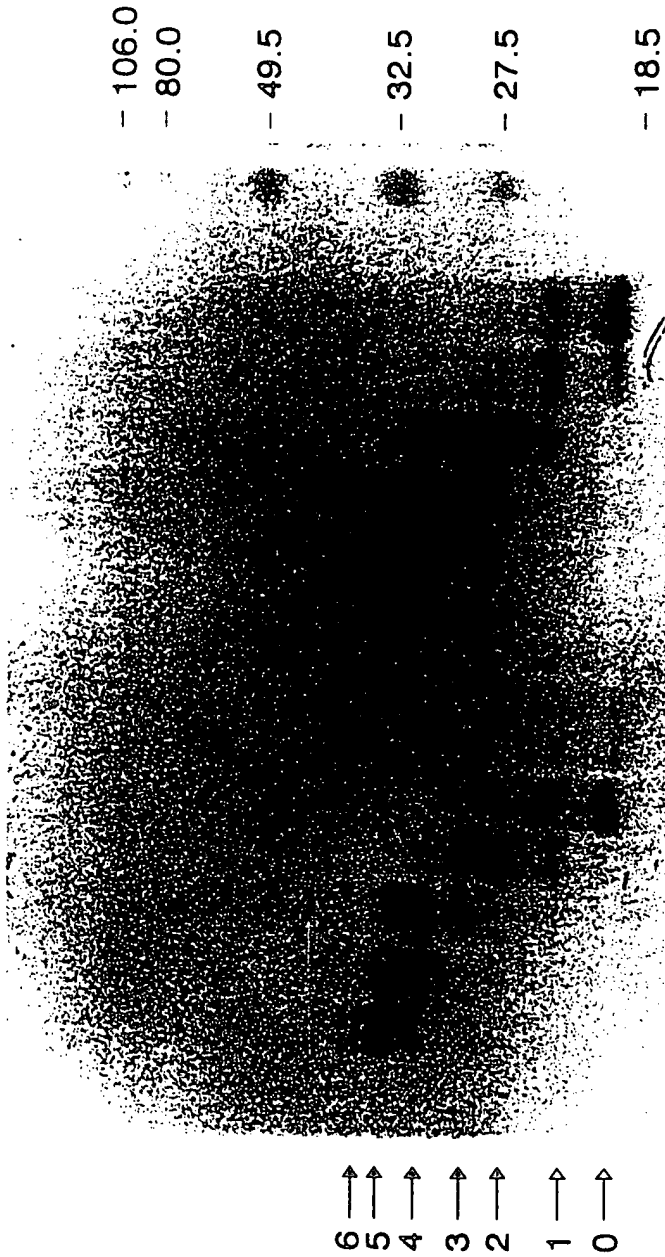


Fig.39

PARTIAL DEGLYCOSYLATION
 OF HCV E1 ENVELOPE PROTEIN

| Endoglycosidase H (Endo H) | Glycopeptidase F (PNGase F) |
|-------------------------------|--------------------------------|
|-------------------------------|--------------------------------|

| | |
|-------|--------|
| 0µg | 0µg |
| 0.6µg | 0.04µg |
| 6µg | 4µg |
| 60µg | 40µg |
| 0.6µg | 400µg |



Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 51 of 64
 Atty. Dkt.: 2551-69



PARTIAL TREATMENT OF HCV E2\E2s ENVELOPE PROTEINS BY PNGase F

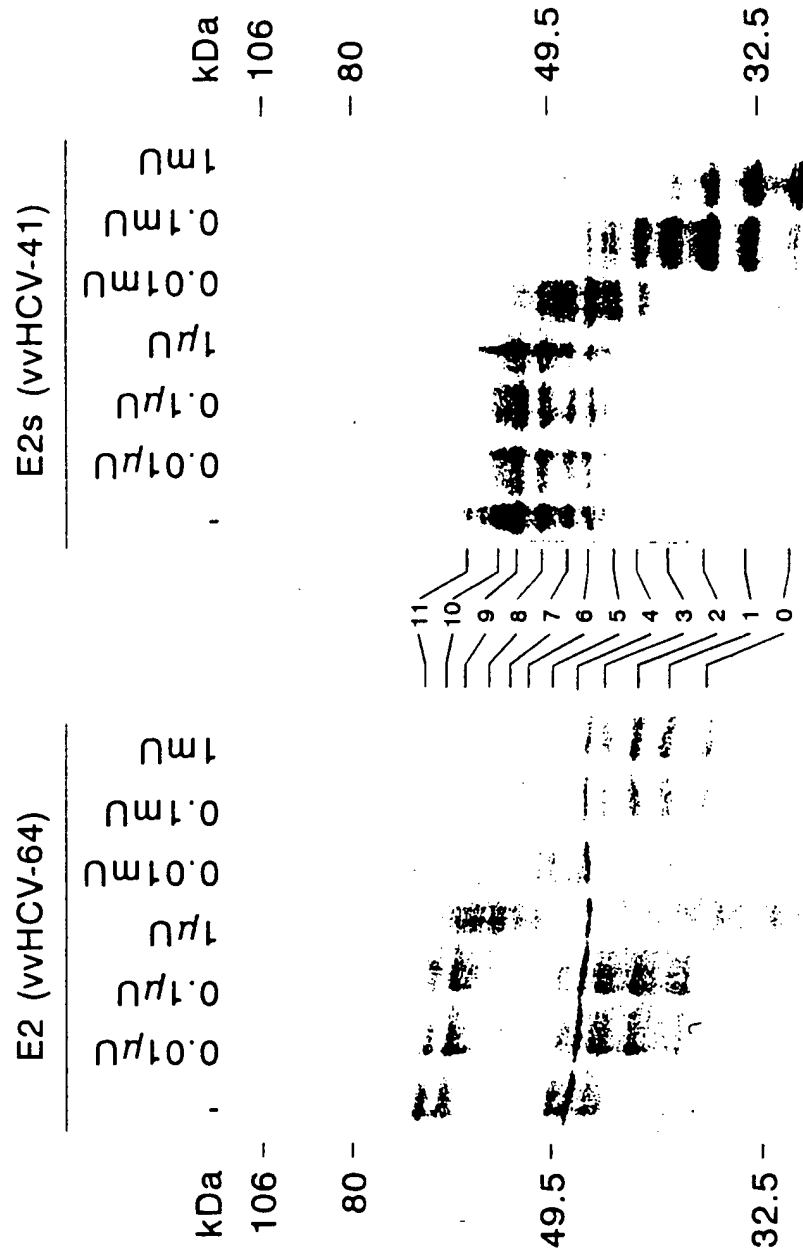


Fig. 40

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 52 of 64
 Atty. Dkt.: 2551-69

In vitro mutagenesis of HCV E1 glycoprotein

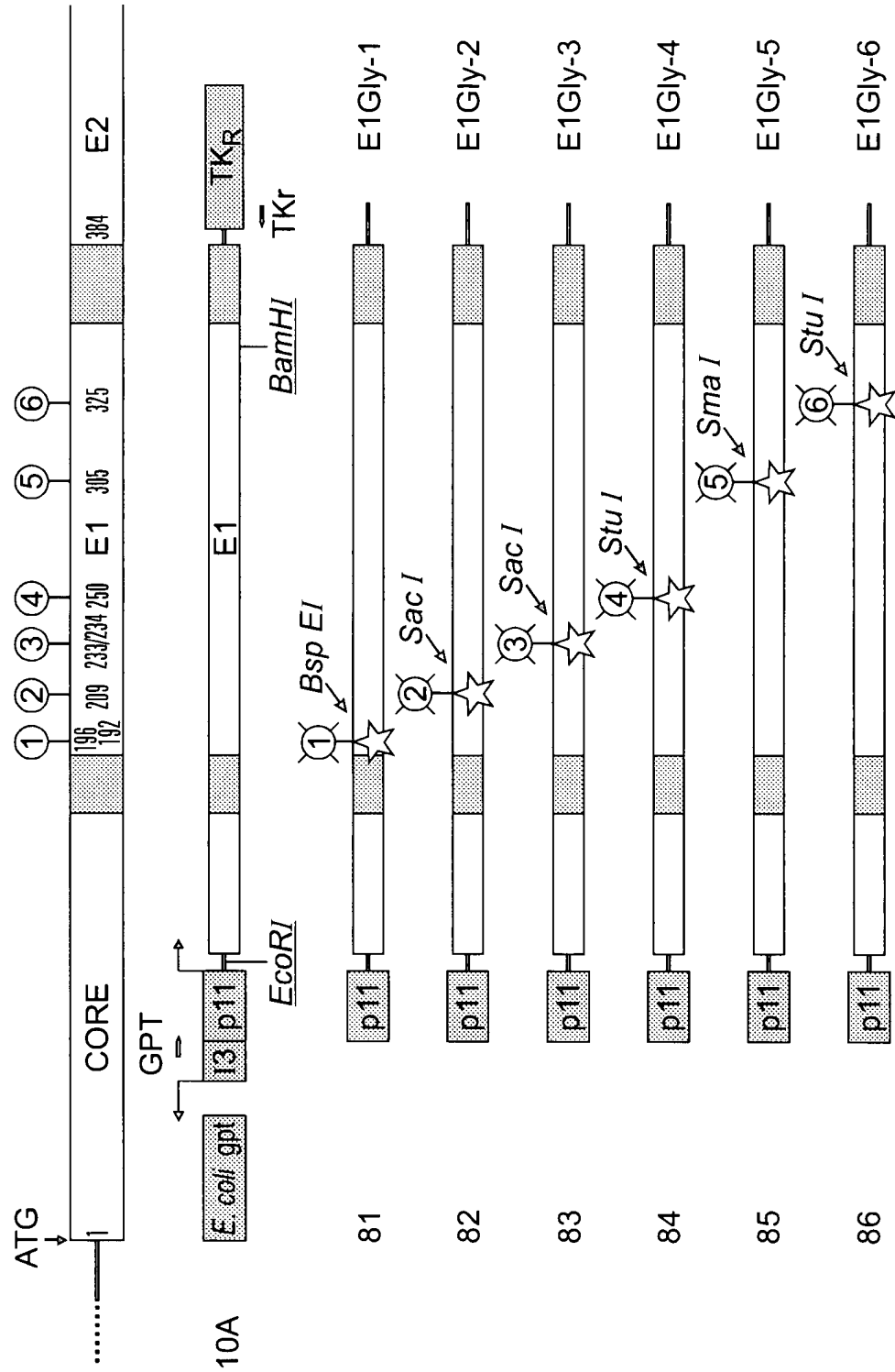


Figure 41

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 53 of 64
 Atty. Dkt.: 2551-69



In vitro mutagenesis of HCV E1 glycoprotein

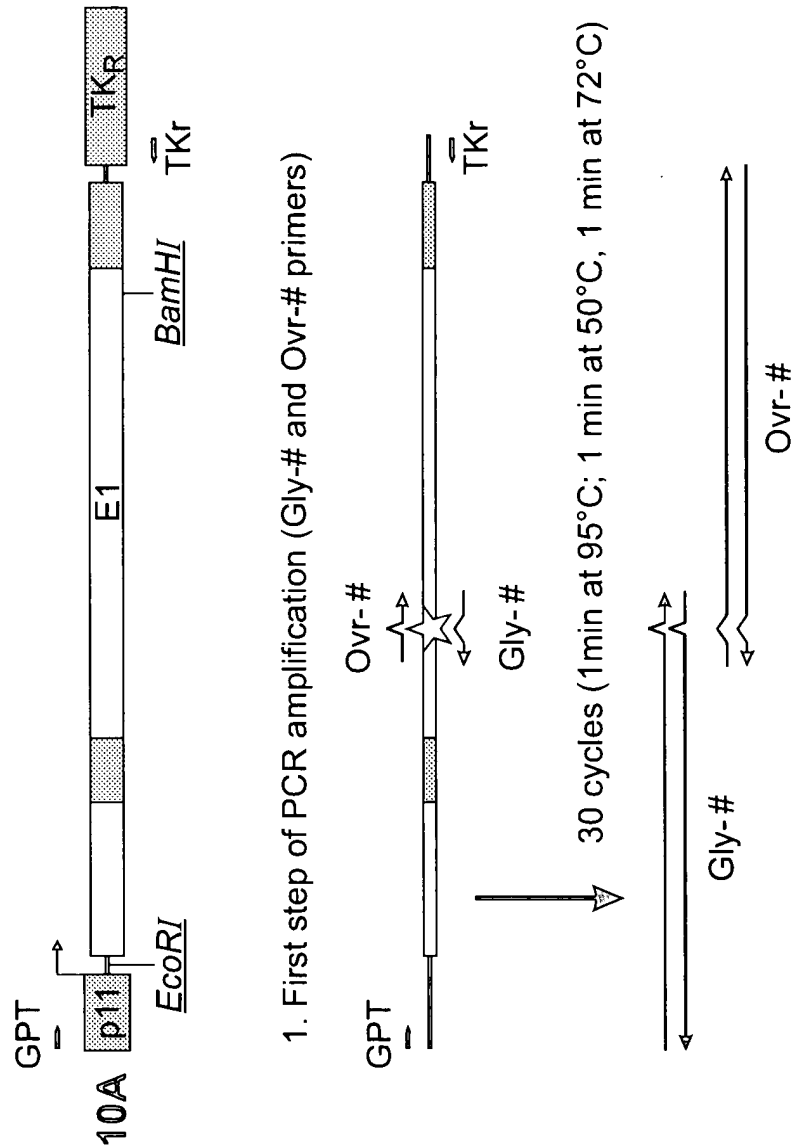


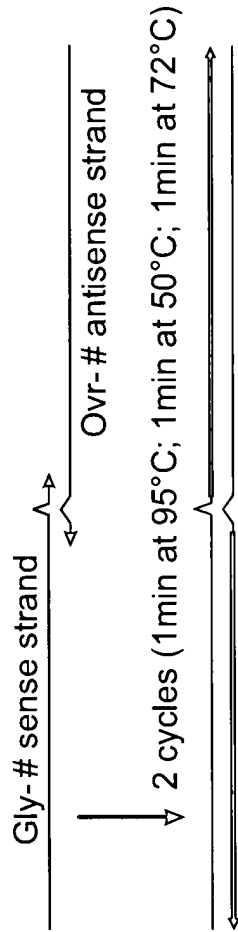
Figure 42A

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 54 of 64
 Atty. Dkt.: 2551-69



2. Overlap extension and nested PCR

a. Overlap extension



b. Nested PCR amplification (GPT-2 and TKr-2 primers)

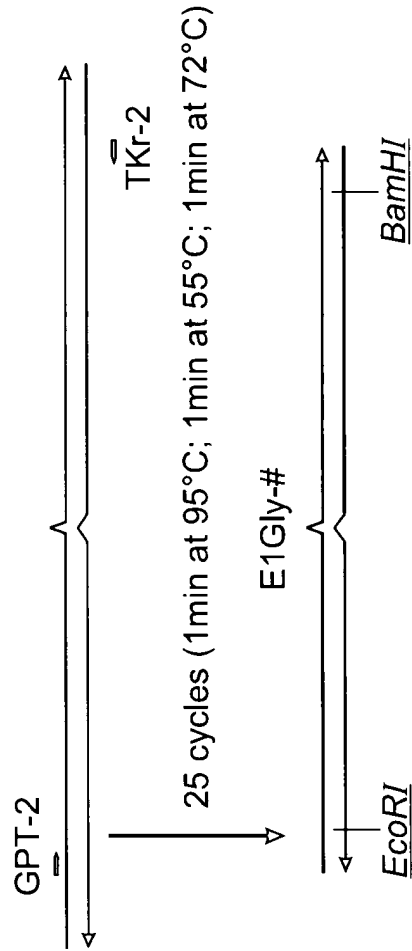


Figure 42B

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 55 of 64
 Atty. Dkt.: 2551-69



In vitro mutagenesis of HCV E1 glycoprotein

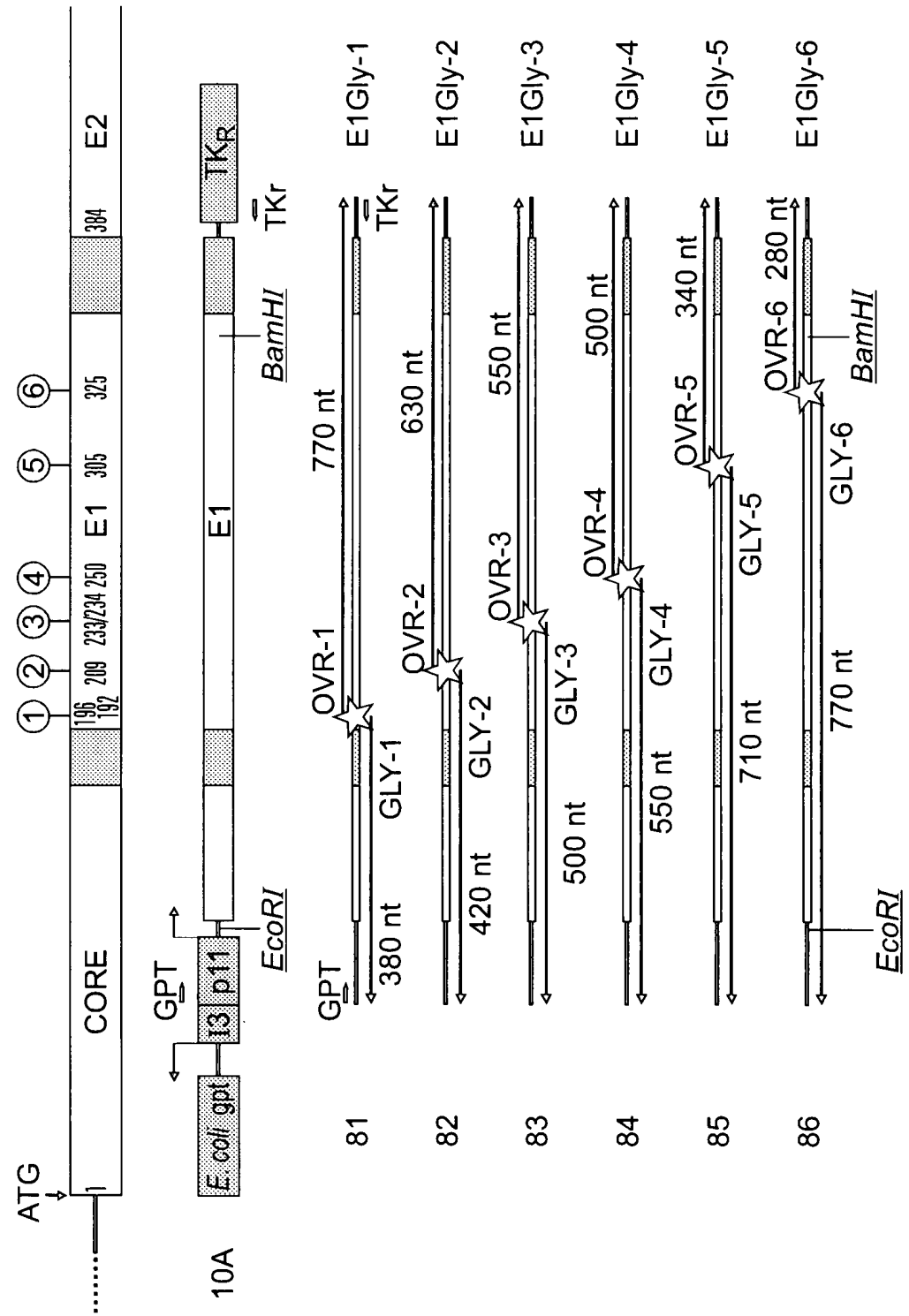


Figure 43

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 56 of 64
 Atty. Dkt.: 2551-69

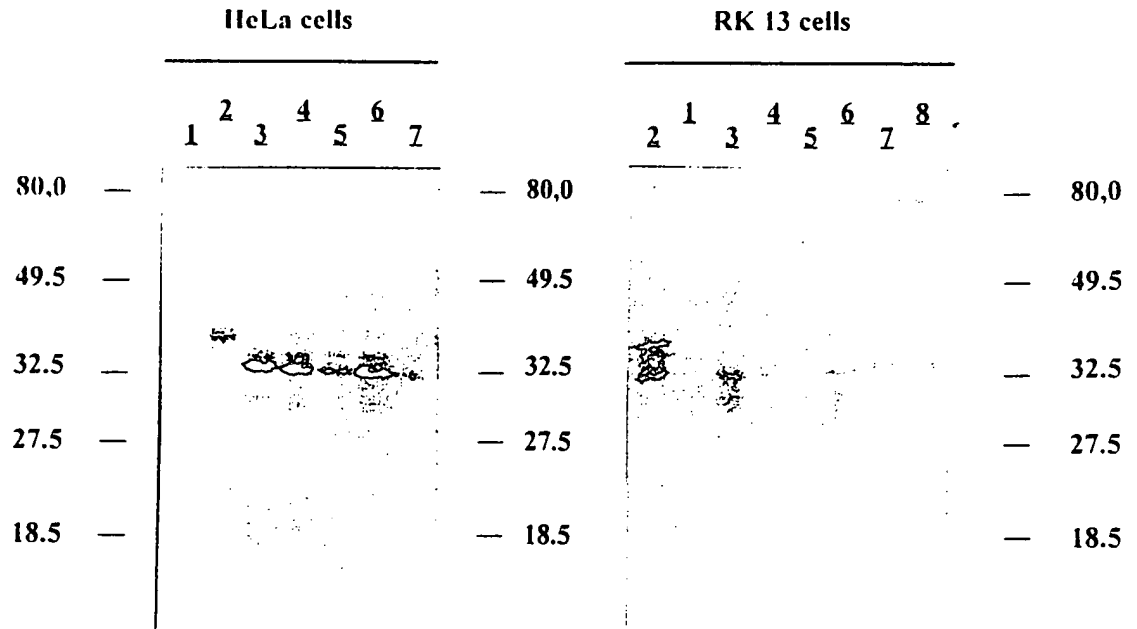


Fig. 44A

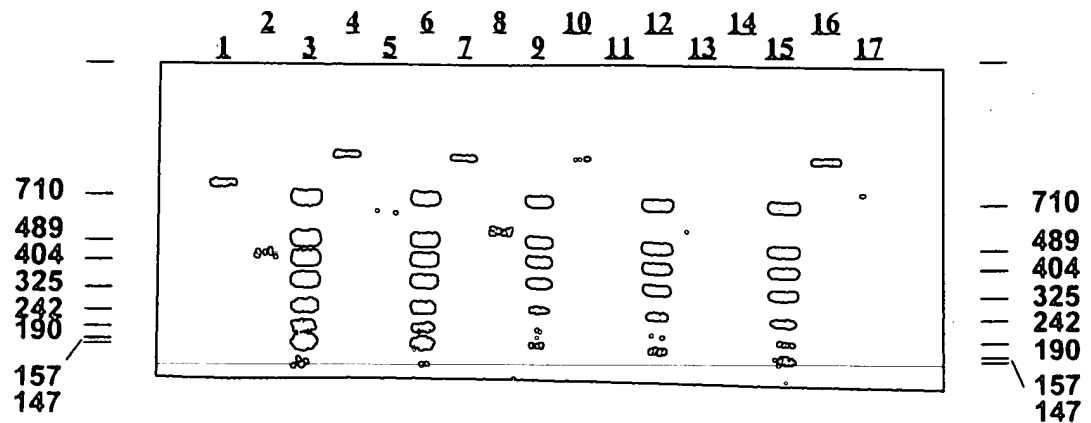


Fig. 44B

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 57 of 64
Atty. Dkt.: 2551-69

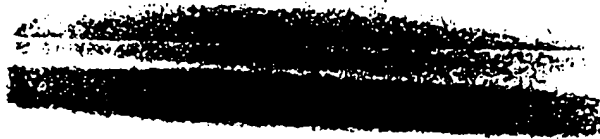


Fig. 45

KDa 119 67 43 29 18
| | | | |



Fig. 46

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 58 of 64
 Atty. Dkt.: 2551-69



| | age (years) | HCV infection (years) | genotype |
|--------|----------------|--------------------------|----------|
| Marcel | 17 | 9 | 1a |
| Peggy | 21 | 16,5 | 1b |
| Femma | 15 | 9 | 1a |
| Yoran | 12 | none | |
| Marti | 12 | none | |

chronic carriers (strong T-cell adjuvant)

↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ 50 µg E1 dose

0 3 6 9 12 15 26 29 32 35 38 41 weeks

naive (alum)

↓ ↓ ↓ ↓ ↓ ↓ 50 µg E1 dose

0 3 6 9 12 15 weeks

Figure 47

Inventor: MAERTENS, et al.
 SN 09/995,860/Sheet 59 of 64
 Atty. Dkt.: 2551-69

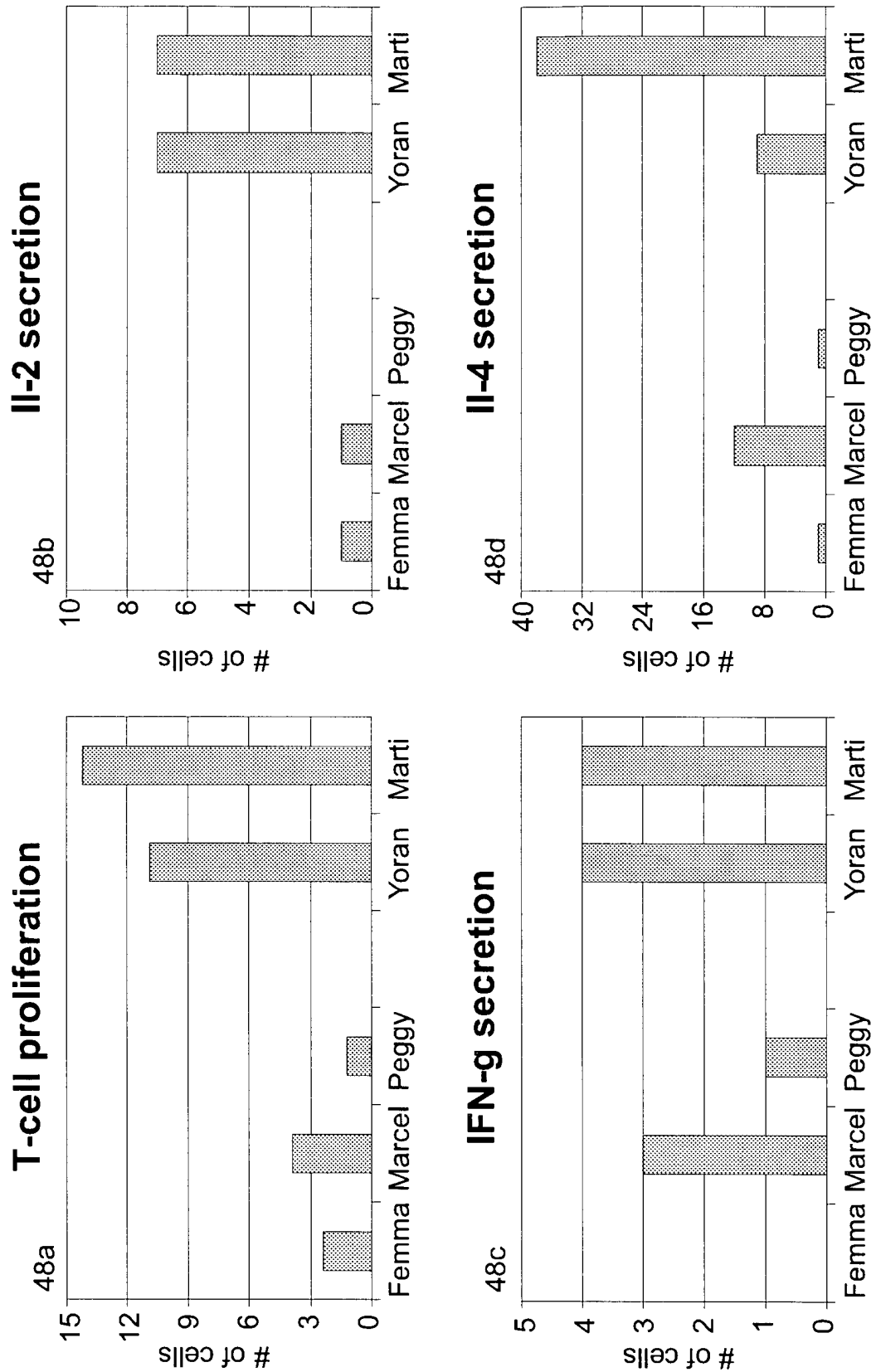
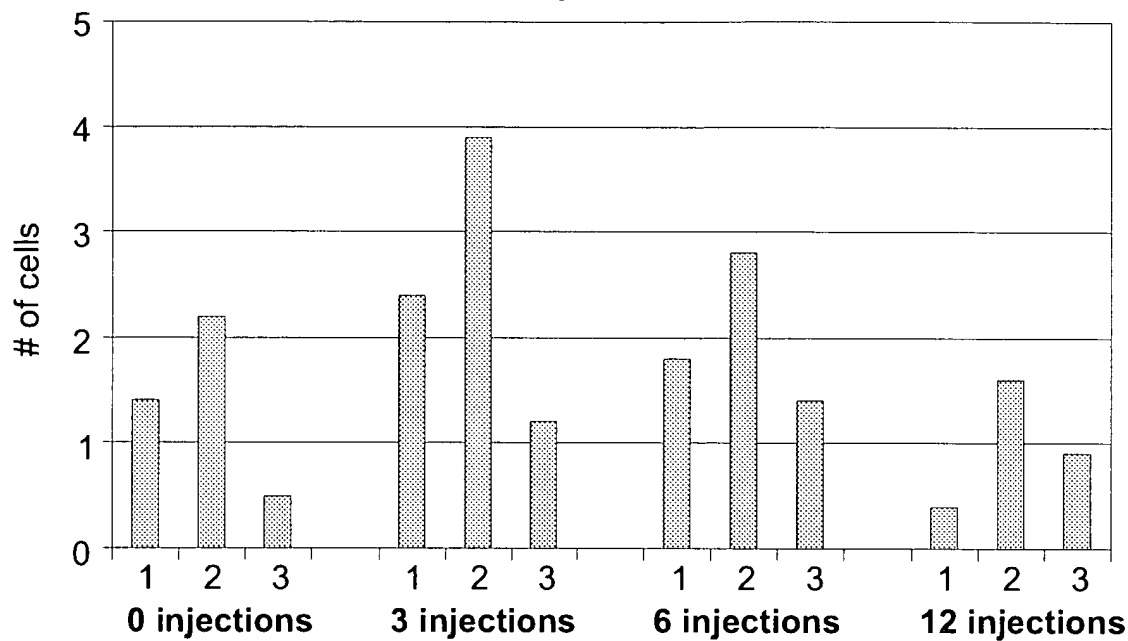


Figure 48

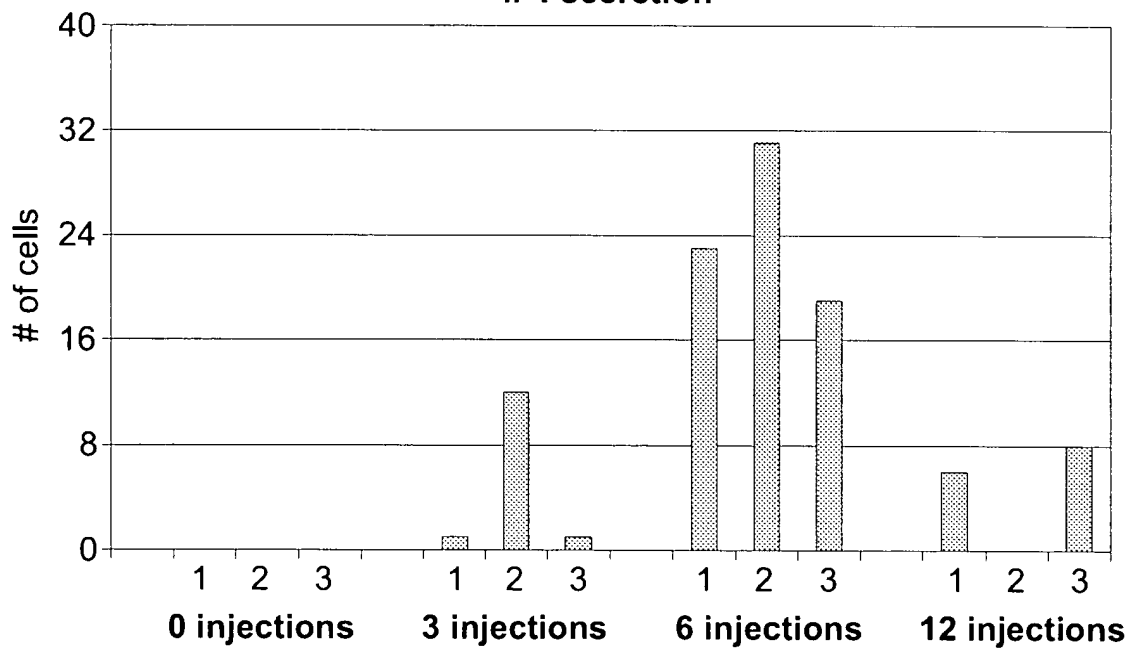
Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 60 of 64
Atty. Dkt.: 2551-69



T-cell proliferation



IL-4 secretion



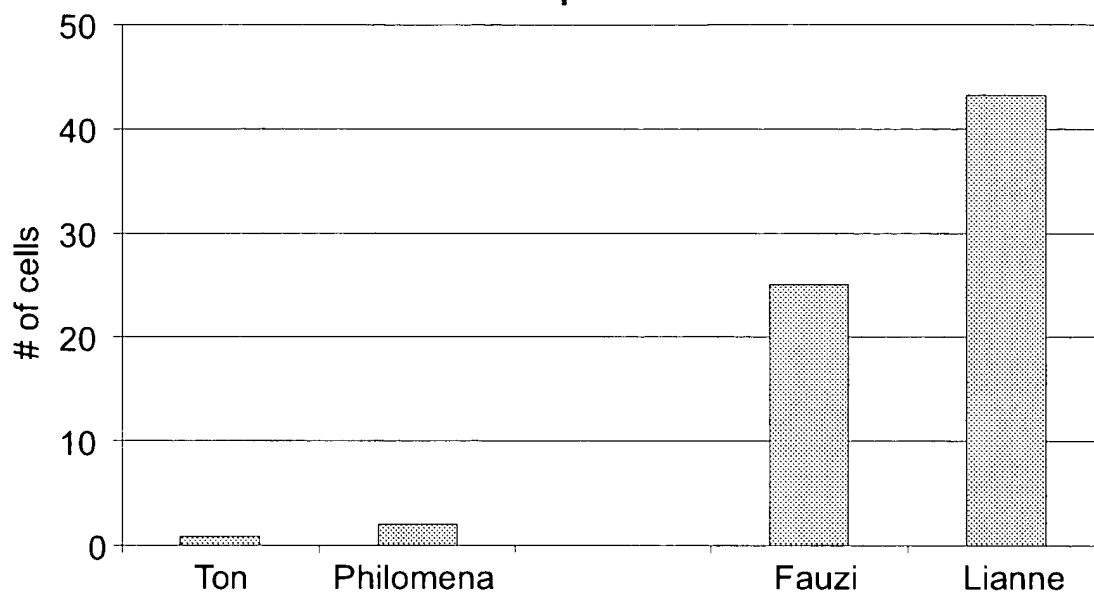
1: Femma, 2: Marcel, 3: Peggy

Figure 49

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 61 of 64
Atty. Dkt.: 2551-69



T-cell proliferation



Il-2 secretion

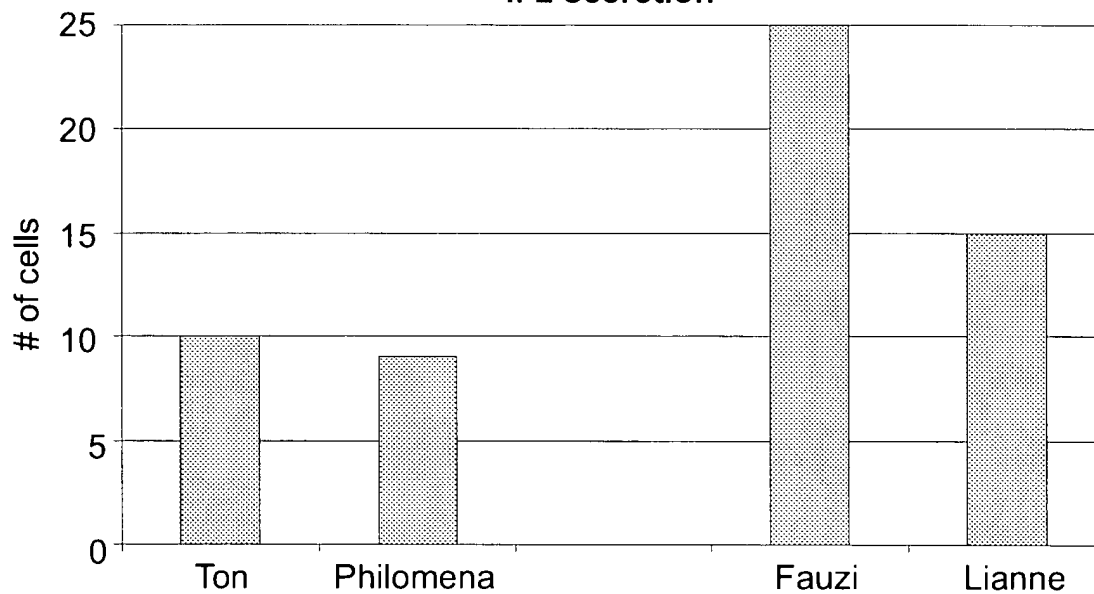


Figure 50

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 62 of 64
Atty. Dkt.: 2551-69

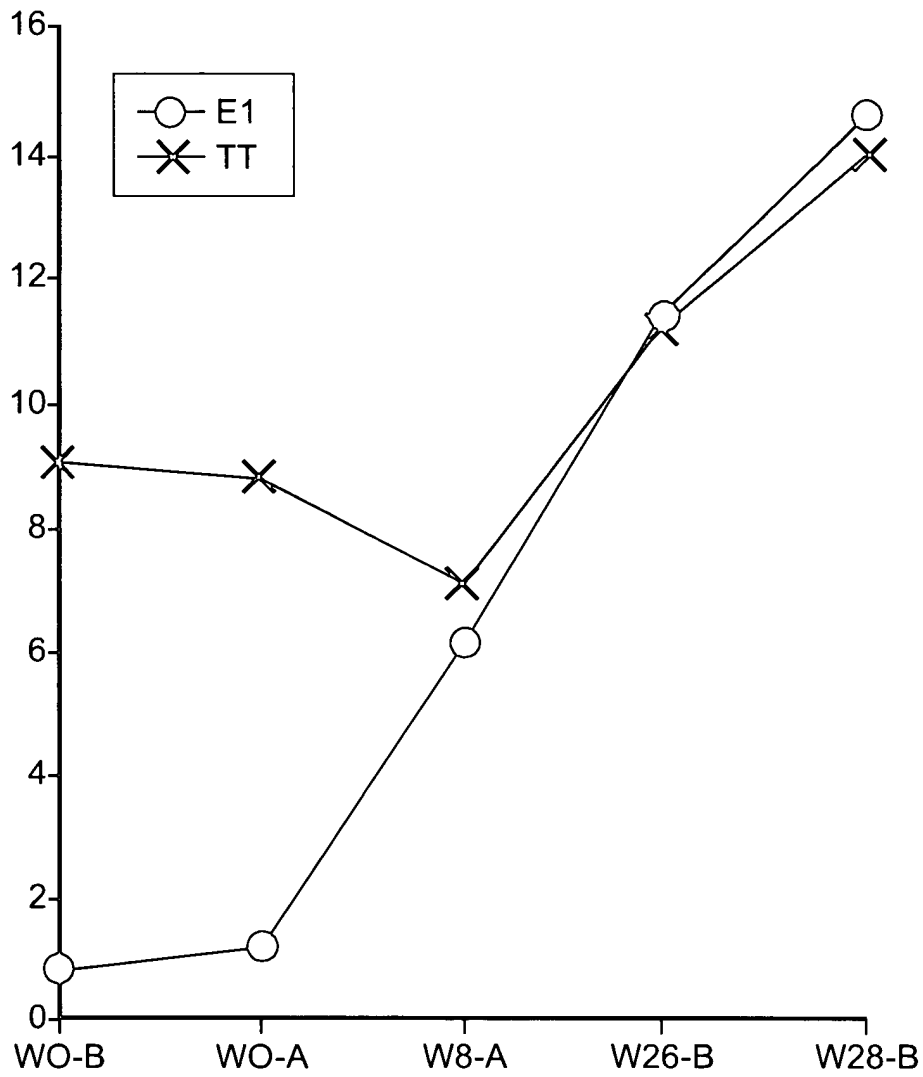


Figure 51

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 63 of 64
Atty. Dkt.: 2551-69

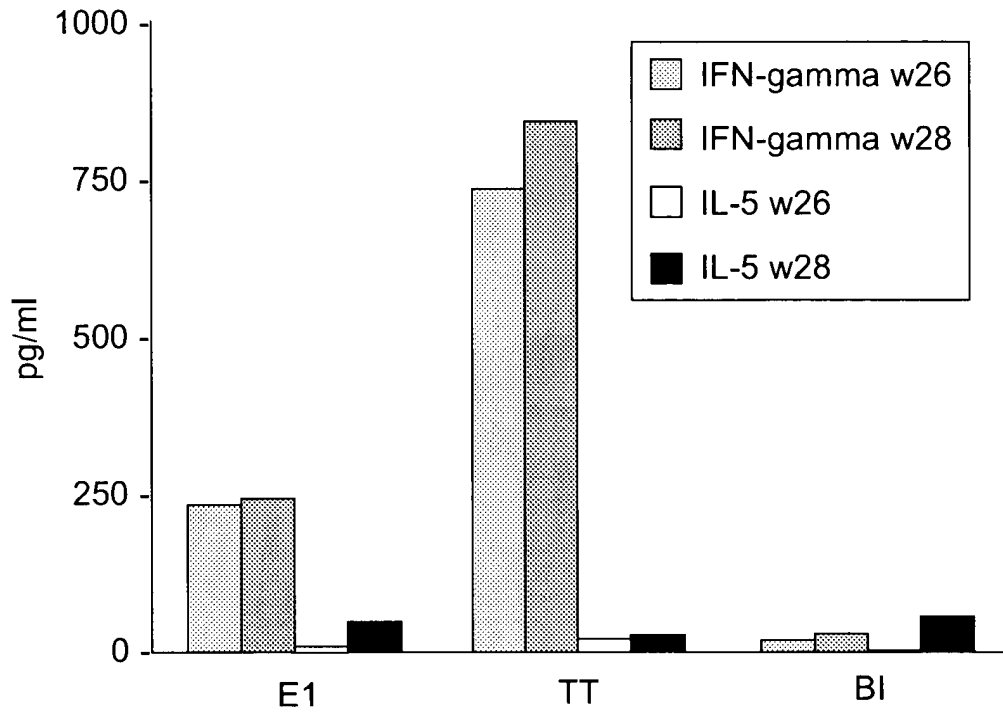


Figure 52

Inventor: MAERTENS, et al.
SN 09/995,860/Sheet 64 of 64
Atty. Dkt.: 2551-69

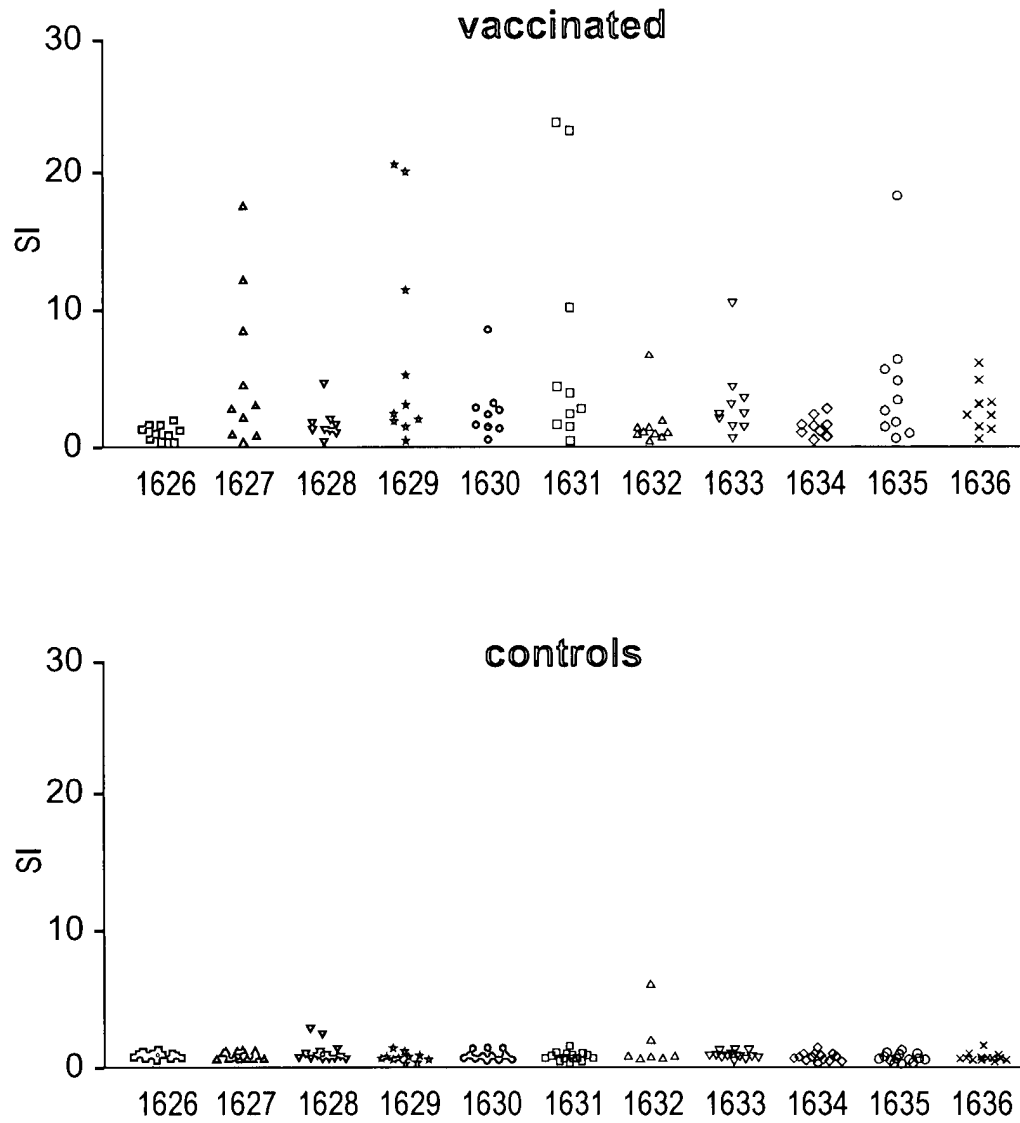


Figure 53